

SEQUENCE LISTING

- <110> Genentech, Inc.
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Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
- <120> Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
- <130> 10466-14
- <140> 09/665,350
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- <150> PCT/US00/04414
<151> 2000-02-22
- <150> US 60/143,048
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- <150> US 60/145,698
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- <150> US 60/146,222
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- <150> PCT/US99/20594
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- <150> PCT/US99/20944
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<211> 353

<212> PRT

<213> Homo sapiens

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Arg Cys Arg Gly Leu Val Asp Lys Phe Asn Gln Gly Met Val Asp Thr
      35              40              45

```

```

Ala Lys Lys Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Lys Thr
      50              55              60

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Leu Ser Lys Tyr Glu Ser Ser Glu Ile Arg Leu Leu Glu Ile Leu Glu
      65              70              75              80

```

```

Gly Leu Cys Glu Ser Ser Asp Phe Glu Cys Asn Gln Met Leu Glu Ala
          85              90              95

```

```

Gln Glu Glu His Leu Glu Ala Trp Trp Leu Gln Leu Lys Ser Glu Tyr
      100              105              110

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```

Pro Asp Leu Phe Glu Trp Phe Cys Val Lys Thr Leu Lys Val Cys Cys
      115              120              125

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Ser Pro Gly Thr Tyr Gly Pro Asp Cys Leu Ala Cys Gln Gly Gly Ser
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Gln Arg Pro Cys Ser Gly Asn Gly His Cys Ser Gly Asp Gly Ser Arg
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 Gln Gly Asp Gly Ser Cys Arg Cys His Met Gly Tyr Gln Gly Pro Leu
 165 170 175
 Cys Thr Asp Cys Met Asp Gly Tyr Phe Ser Ser Leu Arg Asn Glu Thr
 180 185 190
 His Ser Ile Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly
 195 200 205
 Leu Thr Asn Arg Asp Cys Gly Glu Cys Glu Val Gly Trp Val Leu Asp
 210 215 220
 Glu Gly Ala Cys Val Asp Val Asp Glu Cys Ala Ala Glu Pro Pro Pro
 225 230 235 240
 Cys Ser Ala Ala Gln Phe Cys Lys Asn Ala Asn Gly Ser Tyr Thr Cys
 245 250 255
 Glu Glu Cys Asp Ser Ser Cys Val Gly Cys Thr Gly Glu Gly Pro Gly
 260 265 270
 Asn Cys Lys Glu Cys Ile Ser Gly Tyr Ala Arg Glu His Gly Gln Cys
 275 280 285
 Ala Asp Val Asp Glu Cys Ser Leu Ala Glu Lys Thr Cys Val Arg Lys
 290 295 300
 Asn Glu Asn Cys Tyr Asn Thr Pro Gly Ser Tyr Val Cys Val Cys Pro
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 340 345 350
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<210> 3
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 <213> Homo sapiens

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<211> 379

<212> PRT

<213> Homo sapiens

<400> 4

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 20 25 30

Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu
 35 40 45

Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
 50 55 60

Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile

Gly Ala Gln Leu Arg Gln His Thr Pro Ser Leu Lys Lys Ala Glu Glu
 355 360 365

Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp
 370 375

<210> 5

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

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<210> 6

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 6

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21

<210> 7

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 7

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22

<210> 8

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 8

cccacgatgt atgaatggtg gactttgtgt gactcctggt ttctgcatc

49

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<210> 9
 <211> 22
 <212> DNA
 <213> Artificial Sequence

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 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 9
 aaagacgcat ctgcgagtgt cc 22

<210> 10
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 10
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<210> 11
 <211> 2197
 <212> DNA
 <213> Homo sapiens

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 <213> Homo sapiens

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 <223> a, t, c or g

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 <223> a, t, c or g

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 <223> a, t, c or g

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 <222> (144)
 <223> a, t, c or g

<220>
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 <223> a, t, c or g

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 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 14

ttcgaggcct ctgagaagtg gccc

24

<210> 15

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 15

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22

<210> 16

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 16

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<210> 17

<211> 960

<212> DNA

<213> Homo sapiens

<400> 17

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<210> 18

<211> 189

<212> PRT

<213> Homo sapiens

<400> 18

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Thr Pro Thr Cys Ala Thr Pro Ala Gly Pro Met Pro Cys Ser Arg Leu
              20              25              30

Pro Pro Ser Leu Arg Cys Ser Leu His Ser Ala Cys Cys Ser Gly Asp
              35              40              45

Pro Ala Ser Tyr Arg Leu Trp Gly Ala Pro Leu Gln Pro Thr Leu Gly
 50              55              60

Val Val Pro Gln Ala Ser Val Pro Leu Leu Thr Asp Leu Ala Gln Trp
 65              70              75              80

Glu Pro Val Leu Val Pro Glu Ala His Pro Asn Ala Ser Leu Thr Met
              85              90              95

Tyr Val Cys Thr Pro Val Pro His Pro Asp Pro Pro Met Ala Leu Ser
              100              105              110

Arg Thr Pro Thr Arg Gln Ile Ser Ser Ser Asp Thr Asp Pro Pro Ala
              115              120              125

Asp Gly Pro Ser Asn Pro Leu Cys Cys Cys Phe His Gly Pro Ala Phe
 130              135              140

Ser Thr Leu Asn Pro Val Leu Arg His Leu Phe Pro Gln Glu Ala Phe
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Pro Ala His Pro Ile Tyr Asp Leu Ser Gln Val Trp Ser Val Val Ser
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<210> 19

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 19

tgctgtgcta ctctgcaaa gccc

24

<210> 20

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 20

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24

<210> 21

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 21

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44

<210> 22

<211> 1200

<212> DNA

<213> Homo sapiens

<400> 22

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<210> 23

<211> 205

<212> PRT

<213> Homo sapiens

<400> 23

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Leu Ile Leu Cys Cys Gln Thr Gln Tyr Val Arg Asp Gln Gly Ala Met
 20 25 30

Thr Asp Gln Leu Ser Arg Arg Gln Ile Arg Glu Tyr Gln Leu Tyr Ser
 35 40 45

Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg Arg Ile Ser Ala
 50 55 60

Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu Ile Val Glu Thr Asp
 65 70 75 80

Thr Phe Gly Ser Arg Val Arg Ile Lys Gly Ala Glu Ser Glu Lys Tyr
 85 90 95

Ile Cys Met Asn Lys Arg Gly Lys Leu Ile Gly Lys Pro Ser Gly Lys
 100 105 110

Ser Lys Asp Cys Val Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr
 115 120 125

Ala Phe Gln Asn Ala Arg His Glu Gly Trp Phe Met Ala Phe Thr Arg
 130 135 140

Gln Gly Arg Pro Arg Gln Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu
 145 150 155 160

Ala His Phe Ile Lys Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn
 165 170 175

His Ala Glu Lys Gln Lys Gln Phe Glu Phe Val Gly Ser Ala Pro Thr
 180 185 190

Arg Arg Thr Lys Arg Thr Arg Arg Pro Gln Pro Leu Thr
 195 200 205

<210> 24

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 24

cagtacgtga gggaccaggg cgccatga

<210> 25

<211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 25
 ccggtgacct gcacgtgctt gcc

24

<210> 26
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<220>
 <221> modified_base
 <222> (21)
 <223> a, t, c or g

<400> 26
 gcggatctgc cgctgctca nctggctcgg catggcgccc t

41

<210> 27
 <211> 2479
 <212> DNA
 <213> Homo sapiens

<400> 27
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 aggacagcag caaagagggc aacacagget gataagacca gagacagcag ggagattatt 120
 ttaccatacg cctcaggac gttccctcta gctggagttc tggacttcaa cagaacccca 180
 tccagtcatt ttgattttgc tgtttatttt ttttttcttt ttctttttcc caccacattg 240
 tatttttatt ccgtacttca gaaatgggccc tacagaccac aaagtggccc agccatgggg 300
 cttttttcct gaagtcttgg cttatcattt ccctggggct ctactcacag gtgtccaaac 360
 tcctggcctg ccctagtgtg tgccgctgcg acaggaactt tgtctactgt aatgagcgaa 420
 gcttgacctc agtgccctctt gggatcccgg agggcgtaac cgtactctac ctccacaaca 480
 accaaattaa taatgctgga tttcctgcag aactgcacaa tgtacagtgc gtgcacacgg 540
 tctacctgta tggcaacca ctggacgaat tccccatgaa ccttcccaag aatgtcagag 600
 ttctccattt gcaggaaaac aatattcaga ccatctcacg ggctgctctt gccagctct 660
 tgaagcttga agagctgcac ctggatgaca actccatata cacagtgggg gtggaagacg 720
 gggccttcct ggaggtatt agcctcaa atgtgtttt gtctaagaat cacctgagca 780
 gtgtgcctgt tgggcttcct gtggacttgc aagagctgag agtggatgaa aatcgaattg 840
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 atctgatcag gctctatttg caggacaacc agataaacca cattcctttg acagccttct 1080
 caaatctgcg taagctggaa cggctggata tatccaacaa ccaactgcgg atgctgactc 1140

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aagggggtttt tgataatctc tccaacctga agcagctcac tgctcggaat aacccttggt 1200
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gcagagaaaag agtgacccca cctatttctg aacggatcca gctctctatc cattttgtga 1560
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tctttgcttt ttaaatctt 2479

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<210> 28

<211> 660

<212> PRT

<213> Homo sapiens

<400> 28

Met Gly Leu Gln Thr Thr Lys Trp Pro Ser His Gly Ala Phe Phe Leu
1 5 10 15

Lys Ser Trp Leu Ile Ile Ser Leu Gly Leu Tyr Ser Gln Val Ser Lys
20 25 30

Leu Leu Ala Cys Pro Ser Val Cys Arg Cys Asp Arg Asn Phe Val Tyr
35 40 45

Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly Ile Pro Glu Gly
50 55 60

Val Thr Val Leu Tyr Leu His Asn Asn Gln Ile Asn Asn Ala Gly Phe
65 70 75 80

Pro Ala Glu Leu His Asn Val Gln Ser Val His Thr Val Tyr Leu Tyr
85 90 95

Gly Asn Gln Leu Asp Glu Phe Pro Met Asn Leu Pro Lys Asn Val Arg
100 105 110

Val Leu His Leu Gln Glu Asn Asn Ile Gln Thr Ile Ser Arg Ala Ala
115 120 125

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ala | Gln | Leu | Leu | Lys | Leu | Glu | Glu | Leu | His | Leu | Asp | Asp | Asn | Ser |
| 130 | | | | | | 135 | | | | | | 140 | | | |
| Ile | Ser | Thr | Val | Gly | Val | Glu | Asp | Gly | Ala | Phe | Arg | Glu | Ala | Ile | Ser |
| 145 | | | | | | 150 | | | | | | 155 | | | |
| Leu | Lys | Leu | Leu | Phe | Leu | Ser | Lys | Asn | His | Leu | Ser | Ser | Val | Pro | Val |
| | | | 165 | | | | | | 170 | | | 175 | | | |
| Gly | Leu | Pro | Val | Asp | Leu | Gln | Glu | Leu | Arg | Val | Asp | Glu | Asn | Arg | Ile |
| | | | 180 | | | | | | 185 | | | 190 | | | |
| Ala | Val | Ile | Ser | Asp | Met | Ala | Phe | Gln | Asn | Leu | Thr | Ser | Leu | Glu | Arg |
| 195 | | | | | | 200 | | | | | | 205 | | | |
| Leu | Ile | Val | Asp | Gly | Asn | Leu | Leu | Thr | Asn | Lys | Gly | Ile | Ala | Glu | Gly |
| 210 | | | | | | 215 | | | | | | 220 | | | |
| Thr | Phe | Ser | His | Leu | Thr | Lys | Leu | Lys | Glu | Phe | Ser | Ile | Val | Arg | Asn |
| 225 | | | | | | 230 | | | | | | 235 | | | |
| Ser | Leu | Ser | His | Pro | Pro | Pro | Asp | Leu | Pro | Gly | Thr | His | Leu | Ile | Arg |
| | | | 245 | | | | | | 250 | | | 255 | | | |
| Leu | Tyr | Leu | Gln | Asp | Asn | Gln | Ile | Asn | His | Ile | Pro | Leu | Thr | Ala | Phe |
| | | | 260 | | | | | | 265 | | | 270 | | | |
| Ser | Asn | Leu | Arg | Lys | Leu | Glu | Arg | Leu | Asp | Ile | Ser | Asn | Asn | Gln | Leu |
| 275 | | | | | | 280 | | | | | | 285 | | | |
| Arg | Met | Leu | Thr | Gln | Gly | Val | Phe | Asp | Asn | Leu | Ser | Asn | Leu | Lys | Gln |
| 290 | | | | | | 295 | | | | | | 300 | | | |
| Leu | Thr | Ala | Arg | Asn | Asn | Pro | Trp | Phe | Cys | Asp | Cys | Ser | Ile | Lys | Trp |
| 305 | | | | | | 310 | | | | | | 315 | | | |
| Val | Thr | Glu | Trp | Leu | Lys | Tyr | Ile | Pro | Ser | Ser | Leu | Asn | Val | Arg | Gly |
| | | | 325 | | | | | | 330 | | | 335 | | | |
| Phe | Met | Cys | Gln | Gly | Pro | Glu | Gln | Val | Arg | Gly | Met | Ala | Val | Arg | Glu |
| | | | 340 | | | | | | 345 | | | 350 | | | |
| Leu | Asn | Met | Asn | Leu | Leu | Ser | Cys | Pro | Thr | Thr | Thr | Pro | Gly | Leu | Pro |
| 355 | | | | | | 360 | | | | | | 365 | | | |
| Leu | Phe | Thr | Pro | Ala | Pro | Ser | Thr | Ala | Ser | Pro | Thr | Thr | Gln | Pro | Pro |
| 370 | | | | | | 375 | | | | | | 380 | | | |
| Thr | Leu | Ser | Ile | Pro | Asn | Pro | Ser | Arg | Ser | Tyr | Thr | Pro | Pro | Thr | Pro |
| 385 | | | | | | 390 | | | | | | 395 | | | |
| Thr | Thr | Ser | Lys | Leu | Pro | Thr | Ile | Pro | Asp | Trp | Asp | Gly | Arg | Glu | Arg |

<210> 29
<211> 21
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 29

cggtctacct gtatggcaac c

21

<210> 30

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 30

gcaggacaac cagataaacc ac

22

<210> 31

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 31

acgcagattt gagaaggctg tc

22

<210> 32

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 32

ttcacgggct gctcttgccc agctcttgaa gcttgaagag ctgcac

46

<210> 33

<211> 3449

<212> DNA

<213> Homo sapiens

<400> 33

acttggagca agcggcgggc ggggagacag aggcagaggc agaagctggg gctccgtcct 60
cgctcccccac gagcgatccc cgaggagagc cgcggccctc ggcgaggcga agaggccgac 120

| | | | | | | |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| gaggaagacc | cgggtggctg | cgccctgcc | tcgttccca | ggcgccggcg | gctgcagcct | 180 |
| tgccctctt | gctcgcttg | aaaatggaaa | agatgctcgc | aggctgttt | ctgctgatcc | 240 |
| tcggacagat | cgctctctc | cctgccgagg | ccaggggagcg | gtcacgtggg | aggtccatct | 300 |
| ctaggggcag | acacgctcgg | acccacccgc | agacggccct | tctggagagt | tcctgtgaga | 360 |
| acaagcgggc | agacctggtt | ttcatcattg | acagctctcg | cagtgtcaac | acccatgact | 420 |
| atgcaaaggt | caaggagttc | atcgtggaca | tcttgcaatt | cttggacatt | ggctctgatg | 480 |
| tcacccgagt | gggcctgctc | caatatggca | gcactgtcaa | gaatgagttc | tcctcaaga | 540 |
| ccttcaagag | gaagtccgag | gtggagcgtg | ctgtcaagag | gatgcggcat | ctgtccacgg | 600 |
| gcaccatgac | tgggctggcc | atccagtatg | ccctgaacat | cgcattctca | gaagcagagg | 660 |
| gggcccggcc | cctgagggag | aatgtgccac | gggtcataat | gatcgtgaca | gatggggagac | 720 |
| ctcaggactc | cgtggccgag | gtggctgcta | aggcacggga | cacggggcatc | ctaactcttg | 780 |
| ccattgggtg | gggccaaggta | gacttcaaca | ccttgaagtc | cattgggagt | gagcccatg | 840 |
| aggaccatgt | cttctctgtg | gccaatttca | gccagattga | gacgctgacc | tcctgtttcc | 900 |
| agaagaagtt | gtgcacggcc | cacatgtgca | gcaccctgga | gcataactgt | gccacttct | 960 |
| gcatcaacat | ccttggtca | tacgtctgca | ggtgcaaaca | aggctacatt | ctcaactcgg | 1020 |
| atcagacgac | ttgcagaatc | caggatctgt | gtgccatgga | ggaccacaac | tgtgagcagc | 1080 |
| tctgtgtgaa | tgtgccgggc | tccttcgtct | gccagtgcta | cagtggctac | gccctggctg | 1140 |
| aggatgggaa | gaggtgtgtg | gctgtggact | actgtgcctc | agaaaaccac | ggatgtgaac | 1200 |
| atgagtgtgt | aaatgctgat | ggctcctacc | tttgccagtg | ccatgaagga | tttgctctta | 1260 |
| acccagatga | aaaaacgtgc | acaaggatca | actactgtgc | actgaacaaa | ccgggctgtg | 1320 |
| agcatgagt | cgtcaacatg | gaggagagct | actactgccg | ctgccaccgt | ggctacactc | 1380 |
| tggaccccaa | tggcaaaaacc | tgcagccgag | tggaccactg | tgcacagcag | gaccatggct | 1440 |
| gtgagcagct | gtgtctgaac | acggaggatt | ccttcgtctg | ccagtgtctc | gaaggcttcc | 1500 |
| tcacacacga | ggacctcaag | acctgctccc | gggtggatta | ctgectgtctg | agtgaccatg | 1560 |
| gttgtgaata | ctcctgtgtc | aacatggaca | gatcctttgc | ctgtcagtg | cctgagggac | 1620 |
| acgtgctccg | cagcgatggg | aagacgtgtg | caaaattgga | ctcttgctgt | ctgggggacc | 1680 |
| acggttgtga | acattcgtgt | gtaagcagtg | aagattcggt | tgtgtgccag | tgttttgaag | 1740 |
| gttatatact | ccgtgaagat | ggaaaaacct | gcagaaggaa | agatgtctgc | caagctatag | 1800 |
| accatggctg | tgaacacatt | tgtgtgaaca | gtgacgactc | atacacgtgc | gagtgtttgg | 1860 |
| agggattccg | gctcgctgag | gatgggaaac | gctgccgaag | gaaggatgtc | tgcaaatcaa | 1920 |
| cccaccatgg | ctgcgaacac | atttgtgtta | ataatgggaa | ttcctacatc | tgcaaatgct | 1980 |
| cagagggatt | tgttctagct | gaggacggaa | gacggtgcaa | gaaatgcact | gaaggcccaa | 2040 |
| ttgacctgg | ctttgtgatc | gatggatcca | agagctttgg | agaaggaat | tttgaggctg | 2100 |
| tgaagcagtt | tgtcatttga | attatagatt | ccttgacaat | ttccccaaa | ggcgctcgag | 2160 |
| tggggctgct | ccagtatccc | acacagtgcc | acacagagtt | cactctgaga | aacttcaact | 2220 |
| cagccaaaga | catgaaaaaa | gccgtggccc | acatgaaata | catgggaaag | ggctctatga | 2280 |
| ctgggctggc | cctgaaacac | atgtttgaga | gaagttttac | ccaaggagaa | ggggccaggc | 2340 |
| ccctttccac | aagggtgcc | agagcagcca | tttgtttcac | cgacggacgg | gctcaggatg | 2400 |
| acgtctccga | gtgggccagt | aaagccaagg | ccaatggtat | cactatgtat | gctgttgggg | 2460 |
| taggaaaagc | cattgaggag | gaactacaag | agattgcctc | tgagcccaca | aacaagcatc | 2520 |
| tcttctatgc | cgaagacttc | agcacaatgg | atgagataag | tgaaaaactc | aagaaaggca | 2580 |
| tctgtgaagc | tctagaagac | tcgatggaa | gacaggactc | tcagcaggg | gaactgccaa | 2640 |
| aaacggtcca | acagccaaca | gaatctgagc | cagtaccat | aaatatccaa | gacctacttt | 2700 |
| cctgtttctaa | ttttgcagtg | caacacagat | atctgtttga | agaagacaat | cttttacggt | 2760 |
| ctacacaaaa | gctttcccat | tcaacaaaac | cttcaggaag | ccctttggaa | gaaaaacacg | 2820 |
| atcaatgcaa | atgtgaaaac | cttataatgt | tccagaacct | tgcaaacgaa | gaagtaagaa | 2880 |
| aattaacaca | gcgcttagaa | gaaatgacac | agagaatgga | agccctggaa | aatcgctga | 2940 |
| gatacagatg | aagattagaa | atcgcgacac | atttgtagt | attgtatcac | ggattacaat | 3000 |
| gaacgcagt | cagagcccca | aagctcaggc | tattgttaaa | tcaataatgt | tgtgaagtaa | 3060 |
| aaacaatcagt | actgagaaac | ctgggtttgcc | acagaacaaa | gacaagaagt | atacataaac | 3120 |
| ttgtataaat | ttatctagga | aaaaaatcct | tcagaattct | aagatgaatt | taccagggtga | 3180 |
| gaatgaataa | gctatgcga | gtattttgta | atatactgtg | gacacaactt | gcttctgcct | 3240 |
| catcctqcct | tagtgtqcaa | tctcatttga | ctatacgata | aagttttgcac | agtcttactt | 3300 |

ctgtagaaca ctggccatag gaaatgctgt tttttgtac tggactttac cttgatatat 3360
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 ttatacaata ttaaaattca ccacttcag 3449

<210> 34

<211> 915

<212> PRT

<213> Homo sapiens

<400> 34

Met Glu Lys Met Leu Ala Gly Cys Phe Leu Leu Ile Leu Gly Gln Ile
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Val Leu Leu Pro Ala Glu Ala Arg Glu Arg Ser Arg Gly Arg Ser Ile
 20 25 30

Ser Arg Gly Arg His Ala Arg Thr His Pro Gln Thr Ala Leu Leu Glu
 35 40 45

Ser Ser Cys Glu Asn Lys Arg Ala Asp Leu Val Phe Ile Ile Asp Ser
 50 55 60

Ser Arg Ser Val Asn Thr His Asp Tyr Ala Lys Val Lys Glu Phe Ile
 65 70 75 80

Val Asp Ile Leu Gln Phe Leu Asp Ile Gly Pro Asp Val Thr Arg Val
 85 90 95

Gly Leu Leu Gln Tyr Gly Ser Thr Val Lys Asn Glu Phe Ser Leu Lys
 100 105 110

Thr Phe Lys Arg Lys Ser Glu Val Glu Arg Ala Val Lys Arg Met Arg
 115 120 125

His Leu Ser Thr Gly Thr Met Thr Gly Leu Ala Ile Gln Tyr Ala Leu
 130 135 140

Asn Ile Ala Phe Ser Glu Ala Glu Gly Ala Arg Pro Leu Arg Glu Asn
 145 150 155 160

Val Pro Arg Val Ile Met Ile Val Thr Asp Gly Arg Pro Gln Asp Ser
 165 170 175

Val Ala Glu Val Ala Ala Lys Ala Arg Asp Thr Gly Ile Leu Ile Phe
 180 185 190

Ala Ile Gly Val Gly Gln Val Asp Phe Asn Thr Leu Lys Ser Ile Gly
 195 200 205

Ser Glu Pro His Glu Asp His Val Phe Leu Val Ala Asn Phe Ser Gln
 210 215 220

Ile Glu Thr Leu Thr Ser Val Phe Gln Lys Lys Leu Cys Thr Ala His

| | | | | | | |
|-----------------|---------------------|-----------------|-----------------|-----|--|-----|
| 225 | | 230 | | 235 | | 240 |
| Met Cys Ser Thr | Leu Glu His Asn Cys | Ala His Phe Cys | Ile Asn Ile | | | |
| | 245 | 250 | 255 | | | |
| Pro Gly Ser Tyr | Val Cys Arg Cys | Lys Gln Gly Tyr | Ile Leu Asn Ser | | | |
| | 260 | 265 | 270 | | | |
| Asp Gln Thr Thr | Cys Arg Ile Gln Asp | Leu Cys Ala Met | Glu Asp His | | | |
| | 275 | 280 | 285 | | | |
| Asn Cys Glu Gln | Leu Cys Val Asn Val | Pro Gly Ser Phe | Val Cys Gln | | | |
| | 290 | 295 | 300 | | | |
| Cys Tyr Ser Gly | Tyr Ala Leu Ala | Glu Asp Gly Lys | Arg Cys Val Ala | | | |
| | 305 | 310 | 315 | | | 320 |
| Val Asp Tyr Cys | Ala Ser Glu Asn His | Gly Cys Glu His | Glu Cys Val | | | |
| | 325 | 330 | 335 | | | |
| Asn Ala Asp Gly | Ser Tyr Leu Cys | Gln Cys His Glu | Gly Phe Ala Leu | | | |
| | 340 | 345 | 350 | | | |
| Asn Pro Asp Glu | Lys Thr Cys Thr | Arg Ile Asn Tyr | Cys Ala Leu Asn | | | |
| | 355 | 360 | 365 | | | |
| Lys Pro Gly Cys | Glu His Glu Cys | Val Asn Met Glu | Glu Ser Tyr Tyr | | | |
| | 370 | 375 | 380 | | | |
| Cys Arg Cys His | Arg Gly Tyr Thr | Leu Asp Pro Asn | Gly Lys Thr Cys | | | |
| | 385 | 390 | 395 | | | 400 |
| Ser Arg Val Asp | His Cys Ala Gln | Gln Asp His Gly | Cys Glu Gln Leu | | | |
| | 405 | 410 | 415 | | | |
| Cys Leu Asn Thr | Glu Asp Ser Phe | Val Cys Gln Cys | Ser Glu Gly Phe | | | |
| | 420 | 425 | 430 | | | |
| Leu Ile Asn Glu | Asp Leu Lys Thr | Cys Ser Arg Val | Asp Tyr Cys Leu | | | |
| | 435 | 440 | 445 | | | |
| Leu Ser Asp His | Gly Cys Glu Tyr | Ser Cys Val Asn | Met Asp Arg Ser | | | |
| | 450 | 455 | 460 | | | |
| Phe Ala Cys Gln | Cys Pro Glu Gly | His Val Leu Arg | Ser Asp Gly Lys | | | |
| | 465 | 470 | 475 | | | 480 |
| Thr Cys Ala Lys | Leu Asp Ser Cys | Ala Leu Gly Asp | His Gly Cys Glu | | | |
| | 485 | 490 | 495 | | | |
| His Ser Cys Val | Ser Ser Glu Asp | Ser Phe Val Cys | Gln Cys Phe Glu | | | |
| | 500 | 505 | 510 | | | |

Gly Tyr Ile Leu Arg Glu Asp Gly Lys Thr Cys Arg Arg Lys Asp Val
 515 520 525
 Cys Gln Ala Ile Asp His Gly Cys Glu His Ile Cys Val Asn Ser Asp
 530 535 540
 Asp Ser Tyr Thr Cys Glu Cys Leu Glu Gly Phe Arg Leu Ala Glu Asp
 545 550 555 560
 Gly Lys Arg Cys Arg Arg Lys Asp Val Cys Lys Ser Thr His His Gly
 565 570 575
 Cys Glu His Ile Cys Val Asn Asn Gly Asn Ser Tyr Ile Cys Lys Cys
 580 585 590
 Ser Glu Gly Phe Val Leu Ala Glu Asp Gly Arg Arg Cys Lys Lys Cys
 595 600 605
 Thr Glu Gly Pro Ile Asp Leu Val Phe Val Ile Asp Gly Ser Lys Ser
 610 615 620
 Leu Gly Glu Glu Asn Phe Glu Val Val Lys Gln Phe Val Thr Gly Ile
 625 630 635 640
 Ile Asp Ser Leu Thr Ile Ser Pro Lys Ala Ala Arg Val Gly Leu Leu
 645 650 655
 Gln Tyr Ser Thr Gln Val His Thr Glu Phe Thr Leu Arg Asn Phe Asn
 660 665 670
 Ser Ala Lys Asp Met Lys Lys Ala Val Ala His Met Lys Tyr Met Gly
 675 680 685
 Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg Ser
 690 695 700
 Phe Thr Gln Gly Glu Gly Ala Arg Pro Leu Ser Thr Arg Val Pro Arg
 705 710 715 720
 Ala Ala Ile Val Phe Thr Asp Gly Arg Ala Gln Asp Asp Val Ser Glu
 725 730 735
 Trp Ala Ser Lys Ala Lys Ala Asn Gly Ile Thr Met Tyr Ala Val Gly
 740 745 750
 Val Gly Lys Ala Ile Glu Glu Glu Leu Gln Glu Ile Ala Ser Glu Pro
 755 760 765
 Thr Asn Lys His Leu Phe Tyr Ala Glu Asp Phe Ser Thr Met Asp Glu
 770 775 780
 Ile Ser Glu Lys Leu Lys Lys Gly Ile Cys Glu Ala Leu Glu Asp Ser
 785 790 795 800

Asp Gly Arg Gln Asp Ser Pro Ala Gly Glu Leu Pro Lys Thr Val Gln
 805 810 815
 Gln Pro Thr Glu Ser Glu Pro Val Thr Ile Asn Ile Gln Asp Leu Leu
 820 825 830
 Ser Cys Ser Asn Phe Ala Val Gln His Arg Tyr Leu Phe Glu Glu Asp
 835 840 845
 Asn Leu Leu Arg Ser Thr Gln Lys Leu Ser His Ser Thr Lys Pro Ser
 850 855 860
 Gly Ser Pro Leu Glu Glu Lys His Asp Gln Cys Lys Cys Glu Asn Leu
 865 870 875 880
 Ile Met Phe Gln Asn Leu Ala Asn Glu Glu Val Arg Lys Leu Thr Gln
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 Arg Leu Glu Glu Met Thr Gln Arg Met Glu Ala Leu Glu Asn Arg Leu
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 Arg Tyr Arg
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<210> 35

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 35

gtgaccctgg ttgtgaatac tcc

23

<210> 36

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 36

acagccatgg tctatagctt gg

22

<210> 37

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 37

gcctgtcagt gtcctgaggg acacgtgctc cgcagcgatg ggaag

45

<210> 38

<211> 1813

<212> DNA

<213> Homo sapiens

<400> 38

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<210> 39

<211> 390

<212> PRT

<213> Homo sapiens

<400> 39

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| | | | |
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| Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg Ala Gln Leu Gln | 20 | 25 | 30 |
| Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly Gly Glu Val | 35 | 40 | 45 |
| Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln | 50 | 55 | 60 |
| Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys | 65 | 70 | 75 |
| Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro | 85 | 90 | 95 |
| Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg | 100 | 105 | 110 |
| Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val | 115 | 120 | 125 |
| Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr | 130 | 135 | 140 |
| Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro Pro Ser Cys Arg Leu | 145 | 150 | 155 |
| Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser | 165 | 170 | 175 |
| Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro | 180 | 185 | 190 |
| Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser | 195 | 200 | 205 |
| Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys | 210 | 215 | 220 |
| Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu | 225 | 230 | 235 |
| Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly | 245 | 250 | 255 |
| Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu Tyr His | 260 | 265 | 270 |
| Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp | 275 | 280 | 285 |

Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile
 290 295 300

Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Arg
 305 310 315 320

Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser
 325 330 335

Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly
 340 345 350

Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser
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Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser
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Gln Ala Gly Ser Leu Val
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<210> 40

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 40

agggctctcca ggagaaagac tc

22

<210> 41

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 41

attgtgggcc ttgcagacat agac

24

<210> 42

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 42
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 <210> 43
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 43
 gtgtgacaca gcgtgggc 18

 <210> 44
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 44
 gaccggcagg cttctgcg 18

 <210> 45
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 45
 cagcagcttc agccaccagg agtgg 25

 <210> 46
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 46
 ctgagccgtg ggctgcagtc tcgc 24

 <210> 47

<211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 47
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<210> 48
 <211> 2822
 <212> DNA
 <213> Homo sapiens

<400> 48
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<210> 49

<211> 690

<212> PRT

<213> Homo sapiens

<400> 49

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Ser Tyr Thr Gln Asn Cys Thr Lys Thr Pro Cys Leu Pro Asn Ala Lys
      20              25              30

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Cys Glu Ile Arg Asn Gly Ile Glu Ala Cys Tyr Cys Asn Met Gly Phe
      35              40              45

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Ser Gly Asn Gly Val Thr Ile Cys Glu Asp Asp Asn Glu Cys Gly Asn
      50              55              60

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Leu Thr Gln Ser Cys Gly Glu Asn Ala Asn Cys Thr Asn Thr Glu Gly
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Ser Tyr Tyr Cys Met Cys Val Pro Gly Phe Arg Ser Ser Ser Asn Gln
      85              90              95

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Asp Arg Phe Ile Thr Asn Asp Gly Thr Val Cys Ile Glu Asn Val Asn
      100              105              110

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Ala Asn Cys His Leu Asp Asn Val Cys Ile Ala Ala Asn Ile Asn Lys
      115              120              125

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Thr Leu Thr Lys Ile Arg Ser Ile Lys Glu Pro Val Ala Leu Leu Gln
      130              135              140

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Glu Val Tyr Arg Asn Ser Val Thr Asp Leu Ser Pro Thr Asp Ile Ile
      145              150              155              160

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Thr Tyr Ile Glu Ile Leu Ala Glu Ser Ser Ser Leu Leu Gly Tyr Lys
      165              170              175

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Asn Asn Thr Ile Ser Ala Lys Asp Thr Leu Ser Asn Ser Thr Leu Thr

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[illegible]

Asn Leu Cys Cys Ser Leu Phe Leu Ala Glu Leu Val Phe Leu Val Gly
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 Ile Asn Thr Asn Thr Asn Lys Leu Phe Cys Ser Ile Ile Ala Gly Leu
 485 490 495
 Leu His Tyr Phe Phe Leu Ala Ala Phe Ala Trp Met Cys Ile Glu Gly
 500 505 510
 Ile His Leu Tyr Leu Ile Val Val Gly Val Ile Tyr Asn Lys Gly Phe
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 Leu His Lys Asn Phe Tyr Ile Phe Gly Tyr Leu Ser Pro Ala Val Val
 530 535 540
 Val Gly Phe Ser Ala Ala Leu Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys
 545 550 555 560
 Val Cys Trp Leu Ser Thr Glu Asn Asn Phe Ile Trp Ser Phe Ile Gly
 565 570 575
 Pro Ala Cys Leu Ile Ile Leu Val Asn Leu Leu Ala Phe Gly Val Ile
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 Ile Tyr Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro Glu Val Ser
 595 600 605
 Cys Phe Glu Asn Ile Arg Ser Cys Ala Arg Gly Ala Leu Ala Leu Leu
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 Gly Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln
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 Leu Arg
 690

<210> 50

<211> 589

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (61)

<223> a, t, c or g

<400> 50

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<210> 51

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 51

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<210> 52

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 52

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<210> 53

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 53

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<210> 54

<211> 18

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 54

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<210> 55

<211> 18

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 55

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18

<210> 56

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 56

cctagttgag tgatccttgt aag

23

<210> 57

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

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<210> 58

<211> 2137

<212> DNA

<213> Homo sapiens

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<210> 59

<211> 216

<212> PRT

<213> Homo sapiens

<400> 59

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Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro
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His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr
      35                      40                      45

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Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala
      50                      55                      60

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Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu
65 70 75 80

Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His
85 90 95

Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu
100 105 110

Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Glu Ile Arg Pro
115 120 125

Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser
130 135 140

Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu
145 150 155 160

Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro
165 170 175

Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu
180 185 190

Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala
195 200 205

Val Arg Ser Pro Ser Phe Glu Lys
210 215

<210> 60

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 60

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26

<210> 61

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 61

gcctcccggg ctccctgagc agtgccaaac agcggcagtg ta

42

<210> 62
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 62
 ccagtccggt gacaagccca aa 22

<210> 63
 <211> 1295
 <212> DNA
 <213> Homo sapiens

<400> 63
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 tagtgcccca tctgagcaag gccaaaacct ggaagaggat acagtcactc tgggaagtatt 480
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<210> 64
 <211> 312
 <212> PRT
 <213> Homo sapiens

<400> 64
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 20 25 30

Lys Asp Gln Gln Val Val Thr Ala Val Glu Tyr Gln Glu Ala Ile Leu
 35 40 45
 Ala Cys Lys Thr Pro Lys Lys Thr Val Ser Ser Arg Leu Glu Trp Lys
 50 55 60
 Lys Leu Gly Arg Ser Val Ser Phe Val Tyr Tyr Gln Gln Thr Leu Gln
 65 70 75 80
 Gly Asp Phe Lys Asn Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile
 85 90 95
 Lys Asn Val Thr Arg Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser
 100 105 110
 Ala Pro Ser Glu Gln Gly Gln Asn Leu Glu Glu Asp Thr Val Thr Leu
 115 120 125
 Glu Val Leu Val Ala Pro Ala Val Pro Ser Cys Glu Val Pro Ser Ser
 130 135 140
 Ala Leu Ser Gly Thr Val Val Glu Leu Arg Cys Gln Asp Lys Glu Gly
 145 150 155 160
 Asn Pro Ala Pro Glu Tyr Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu
 165 170 175
 Glu Asn Pro Arg Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met
 180 185 190
 Asn Thr Lys Thr Gly Thr Leu Gln Phe Asn Thr Val Ser Lys Leu Asp
 195 200 205
 Thr Gly Glu Tyr Ser Cys Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg
 210 215 220
 Cys Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile
 225 230 235 240
 Ile Ala Ala Val Val Val Val Ala Leu Val Ile Ser Val Cys Gly Leu
 245 250 255
 Gly Val Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser
 260 265 270
 Phe Gln Lys Ser Asn Ser Ser Ser Lys Ala Thr Thr Met Ser Glu Asn
 275 280 285
 Val Gln Trp Leu Thr Pro Val Ile Pro Ala Leu Trp Lys Ala Ala Ala
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 Gly Gly Ser Arg Gly Gln Glu Phe

305

310

<210> 65
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 65
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22

<210> 66
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 66
 acctgcgata tccaacagaa ttg

23

<210> 67
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 67
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48

<210> 68
 <211> 2639
 <212> DNA
 <213> Homo sapiens

<400> 68
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 gcatcatgct gctattcctg caaatactga agaagcatgg gatttaaata ttttacttct 180
 aaataaatga attactcaat ctcctatgac catctataca tactccacct tcaaaaagta 240
 catcaatatt atatcattaa ggaaatagta accttctctt ctccaatag catgacattt 300
 ttggacaatg caattgtggc actggcactt atttcagtga agaaaaactt tgtggttcta 360
 tggcattcat catttgacaa atgcaagcat cttccttata aatcagctcc tattgaactt 420
 actagcactg actgtggaat ccttaagggc ccattacatt tctgaagaag aaagctaaga 480
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aagctgtaga taaaaaagtg gattgtccac gggtatgtac gtgtgaaatc aggccttggt 600
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<210> 69

<211> 708

<212> PRT

<213> Homo sapiens

<400> 69

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20 25 30

Cys Thr Cys Glu Ile Arg Pro Trp Phe Thr Pro Arg Ser Ile Tyr Met
35 40 45

Glu Ala Ser Thr Val Asp Cys Asn Asp Leu Gly Leu Leu Thr Phe Pro
50 55 60

Ala Arg Leu Pro Ala Asn Thr Gln Ile Leu Leu Leu Gln Thr Asn Asn
 65 70 75 80
 Ile Ala Lys Ile Glu Tyr Ser Thr Asp Phe Pro Val Asn Leu Thr Gly
 85 90 95
 Leu Asp Leu Ser Gln Asn Asn Leu Ser Ser Val Thr Asn Ile Asn Val
 100 105 110
 Lys Lys Met Pro Gln Leu Leu Ser Val Tyr Leu Glu Glu Asn Lys Leu
 115 120 125
 Thr Glu Leu Pro Glu Lys Cys Leu Ser Glu Leu Ser Asn Leu Gln Glu
 130 135 140
 Leu Tyr Ile Asn His Asn Leu Leu Ser Thr Ile Ser Pro Gly Ala Phe
 145 150 155 160
 Ile Gly Leu His Asn Leu Leu Arg Leu His Leu Asn Ser Asn Arg Leu
 165 170 175
 Gln Met Ile Asn Ser Lys Trp Phe Asp Ala Leu Pro Asn Leu Glu Ile
 180 185 190
 Leu Met Ile Gly Glu Asn Pro Ile Ile Arg Ile Lys Asp Met Asn Phe
 195 200 205
 Lys Pro Leu Ile Asn Leu Arg Ser Leu Val Ile Ala Gly Ile Asn Leu
 210 215 220
 Thr Glu Ile Pro Asp Asn Ala Leu Val Gly Leu Glu Asn Leu Glu Ser
 225 230 235 240
 Ile Ser Phe Tyr Asp Asn Arg Leu Ile Lys Val Pro His Val Ala Leu
 245 250 255
 Gln Lys Val Val Asn Leu Lys Phe Leu Asp Leu Asn Lys Asn Pro Ile
 260 265 270
 Asn Arg Ile Arg Arg Gly Asp Phe Ser Asn Met Leu His Leu Lys Glu
 275 280 285
 Leu Gly Ile Asn Asn Met Pro Glu Leu Ile Ser Ile Asp Ser Leu Ala
 290 295 300
 Val Asp Asn Leu Pro Asp Leu Arg Lys Ile Glu Ala Thr Asn Asn Pro
 305 310 315 320
 Arg Leu Ser Tyr Ile His Pro Asn Ala Phe Phe Arg Leu Pro Lys Leu
 325 330 335
 Glu Ser Leu Met Leu Asn Ser Asn Ala Leu Ser Ala Leu Tyr His Gly

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| 340 | | | | | | | 345 | | | | | 350 | | | | | |
| Thr | Ile | Glu | Ser | Leu | Pro | Asn | Leu | Lys | Glu | Ile | Ser | Ile | His | Ser | Asn | | |
| 355 | | | | | | | 360 | | | | | 365 | | | | | |
| Pro | Ile | Arg | Cys | Asp | Cys | Val | Ile | Arg | Trp | Met | Asn | Met | Asn | Lys | Thr | | |
| 370 | | | | | | | 375 | | | | | 380 | | | | | |
| Asn | Ile | Arg | Phe | Met | Glu | Pro | Asp | Ser | Leu | Phe | Cys | Val | Asp | Pro | Pro | | |
| 385 | | | | | | | 390 | | | | | 395 | | | | 400 | |
| Glu | Phe | Gln | Gly | Gln | Asn | Val | Arg | Gln | Val | His | Phe | Arg | Asp | Met | Met | | |
| | | | | | | | 405 | | | | | 410 | | | | 415 | |
| Glu | Ile | Cys | Leu | Pro | Leu | Ile | Ala | Pro | Glu | Ser | Phe | Pro | Ser | Asn | Leu | | |
| | | | | | | | 420 | | | | | 425 | | | | 430 | |
| Asn | Val | Glu | Ala | Gly | Ser | Tyr | Val | Ser | Phe | His | Cys | Arg | Ala | Thr | Ala | | |
| | | | | | | | 435 | | | | | 440 | | | | 445 | |
| Glu | Pro | Gln | Pro | Glu | Ile | Tyr | Trp | Ile | Thr | Pro | Ser | Gly | Gln | Lys | Leu | | |
| | | | | | | | 450 | | | | | 455 | | | | 460 | |
| Leu | Pro | Asn | Thr | Leu | Thr | Asp | Lys | Phe | Tyr | Val | His | Ser | Glu | Gly | Thr | | |
| 465 | | | | | | | 470 | | | | | 475 | | | | 480 | |
| Leu | Asp | Ile | Asn | Gly | Val | Thr | Pro | Lys | Glu | Gly | Gly | Leu | Tyr | Thr | Cys | | |
| | | | | | | | 485 | | | | | 490 | | | | 495 | |
| Ile | Ala | Thr | Asn | Leu | Val | Gly | Ala | Asp | Leu | Lys | Ser | Val | Met | Ile | Lys | | |
| | | | | | | | 500 | | | | | 505 | | | | 510 | |
| Val | Asp | Gly | Ser | Phe | Pro | Gln | Asp | Asn | Asn | Gly | Ser | Leu | Asn | Ile | Lys | | |
| | | | | | | | 515 | | | | | 520 | | | | 525 | |
| Ile | Arg | Asp | Ile | Gln | Ala | Asn | Ser | Val | Leu | Val | Ser | Trp | Lys | Ala | Ser | | |
| 530 | | | | | | | 535 | | | | | 540 | | | | | |
| Ser | Lys | Ile | Leu | Lys | Ser | Ser | Val | Lys | Trp | Thr | Ala | Phe | Val | Lys | Thr | | |
| 545 | | | | | | | 550 | | | | | 555 | | | | 560 | |
| Glu | Asn | Ser | His | Ala | Ala | Gln | Ser | Ala | Arg | Ile | Pro | Ser | Asp | Val | Lys | | |
| | | | | | | | 565 | | | | | 570 | | | | 575 | |
| Val | Tyr | Asn | Leu | Thr | His | Leu | Asn | Pro | Ser | Thr | Glu | Tyr | Lys | Ile | Cys | | |
| | | | | | | | 580 | | | | | 585 | | | | 590 | |
| Ile | Asp | Ile | Pro | Thr | Ile | Tyr | Gln | Lys | Asn | Arg | Lys | Lys | Cys | Val | Asn | | |
| 595 | | | | | | | 600 | | | | | 605 | | | | | |
| Val | Thr | Thr | Lys | Gly | Leu | His | Pro | Asp | Gln | Lys | Glu | Tyr | Glu | Lys | Asn | | |
| 610 | | | | | | | 615 | | | | | 620 | | | | | |

Asn Thr Thr Thr Leu Met Ala Cys Leu Gly Gly Leu Leu Gly Ile Ile
625 630 635 640

Gly Val Ile Cys Leu Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp
645 650 655

Gly Gly His Ser Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala
660 665 670

Leu Gly Glu Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys
675 680 685

Glu Lys Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro
690 695 700

Thr Asn Met Ser
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<210> 70
<211> 1305
<212> DNA
<213> Homo sapiens

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cttaactttg aaccatggga aaaaaaaaaa aaaaaaaaaa aaaca 1305

<210> 71
<211> 259
<212> PRT
<213> Homo sapiens

<400> 71

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 Met Cys Pro Lys Gly Cys Leu Cys Ser Ser Ser Gly Gly Leu Asn Val
 35 40 45
 Thr Cys Ser Asn Ala Asn Leu Lys Glu Ile Pro Arg Asp Leu Pro Pro
 50 55 60
 Glu Thr Val Leu Leu Tyr Leu Asp Ser Asn Gln Ile Thr Ser Ile Pro
 65 70 75 80
 Asn Glu Ile Phe Lys Asp Leu His Gln Leu Arg Val Leu Asn Leu Ser
 85 90 95
 Lys Asn Gly Ile Glu Phe Ile Asp Glu His Ala Phe Lys Gly Val Ala
 100 105 110
 Glu Thr Leu Gln Thr Leu Asp Leu Ser Asp Asn Arg Ile Gln Ser Val
 115 120 125
 His Lys Asn Ala Phe Asn Asn Leu Lys Ala Arg Ala Arg Ile Ala Asn
 130 135 140
 Asn Pro Trp His Cys Asp Cys Thr Leu Gln Gln Val Leu Arg Ser Met
 145 150 155 160
 Ala Ser Asn His Glu Thr Ala His Asn Val Ile Cys Lys Thr Ser Val
 165 170 175
 Leu Asp Glu His Ala Gly Arg Pro Phe Leu Asn Ala Ala Asn Asp Ala
 180 185 190
 Asp Leu Cys Asn Leu Pro Lys Lys Thr Thr Asp Tyr Ala Met Leu Val
 195 200 205
 Thr Met Phe Gly Trp Phe Thr Met Val Ile Ser Tyr Val Val Tyr Tyr
 210 215 220
 Val Arg Gln Asn Gln Glu Asp Ala Arg Arg His Leu Glu Tyr Leu Lys
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 Ser Leu Pro Ser Arg Gln Lys Lys Ala Asp Glu Pro Asp Asp Ile Ser
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<210> 72

<211> 2290

<212> DNA

<213> Homo sapiens

<400> 72

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<210> 73

<211> 620

<212> PRT

<213> Homo sapiens

<400> 73

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 Ser Val Leu Ser Gly Ser Ala Thr Gly Cys Pro Pro Arg Cys Glu Cys
 35 40 45
 Ser Ala Gln Asp Arg Ala Val Leu Cys His Arg Lys Cys Phe Val Ala
 50 55 60
 Val Pro Glu Gly Ile Pro Thr Glu Thr Arg Leu Leu Asp Leu Gly Lys
 65 70 75 80
 Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu Phe Ala Ser Phe Pro His
 85 90 95
 Leu Glu Glu Leu Glu Leu Asn Glu Asn Ile Val Ser Ala Val Glu Pro
 100 105 110
 Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg Thr Leu Gly Leu Arg Ser
 115 120 125
 Asn Arg Leu Lys Leu Ile Pro Leu Gly Val Phe Thr Gly Leu Ser Asn
 130 135 140
 Leu Thr Lys Gln Asp Ile Ser Glu Asn Lys Ile Val Ile Leu Leu Asp
 145 150 155 160
 Tyr Met Phe Gln Asp Leu Tyr Asn Leu Lys Ser Leu Glu Val Gly Asp
 165 170 175
 Asn Asp Leu Val Tyr Ile Ser His Arg Ala Phe Ser Gly Leu Asn Ser
 180 185 190
 Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn Leu Thr Ser Ile Pro Thr
 195 200 205
 Glu Ala Leu Ser His Leu His Gly Leu Ile Val Leu Arg Leu Arg His
 210 215 220
 Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser Phe Lys Arg Leu Tyr Arg
 225 230 235 240
 Leu Lys Val Leu Glu Ile Ser His Trp Pro Tyr Leu Asp Thr Met Thr
 245 250 255
 Pro Asn Cys Leu Tyr Gly Leu Asn Leu Thr Ser Leu Ser Ile Thr His
 260 265 270
 Cys Asn Leu Thr Ala Val Pro Tyr Leu Ala Val Arg His Leu Val Tyr
 275 280 285
 Leu Arg Phe Leu Asn Leu Ser Tyr Asn Pro Ile Ser Thr Ile Glu Gly
 290 295 300

Ser Met Leu His Glu Leu Leu Arg Leu Gln Glu Ile Gln Leu Val Gly
 305 310 315 320
 Gly Gln Leu Ala Val Val Glu Pro Tyr Ala Phe Arg Gly Leu Asn Tyr
 325 330 335
 Leu Arg Val Leu Asn Val Ser Gly Asn Gln Leu Thr Thr Leu Glu Glu
 340 345 350
 Ser Val Phe His Ser Val Gly Asn Leu Glu Thr Leu Ile Leu Asp Ser
 355 360 365
 Asn Pro Leu Ala Cys Asp Cys Arg Leu Leu Trp Val Phe Arg Arg Arg
 370 375 380
 Trp Arg Leu Asn Phe Asn Arg Gln Gln Pro Thr Cys Ala Thr Pro Glu
 385 390 395 400
 Phe Val Gln Gly Lys Glu Phe Lys Asp Phe Pro Asp Val Leu Leu Pro
 405 410 415
 Asn Tyr Phe Thr Cys Arg Arg Ala Arg Ile Arg Asp Arg Lys Ala Gln
 420 425 430
 Gln Val Phe Val Asp Glu Gly His Thr Val Gln Phe Val Cys Arg Ala
 435 440 445
 Asp Gly Asp Pro Pro Pro Ala Ile Leu Trp Leu Ser Pro Arg Lys His
 450 455 460
 Leu Val Ser Ala Lys Ser Asn Gly Arg Leu Thr Val Phe Pro Asp Gly
 465 470 475 480
 Thr Leu Glu Val Arg Tyr Ala Gln Val Gln Asp Asn Gly Thr Tyr Leu
 485 490 495
 Cys Ile Ala Ala Asn Ala Gly Gly Asn Asp Ser Met Pro Ala His Leu
 500 505 510
 His Val Arg Ser Tyr Ser Pro Asp Trp Pro His Gln Pro Asn Lys Thr
 515 520 525
 Phe Ala Phe Ile Ser Asn Gln Pro Gly Glu Gly Glu Ala Asn Ser Thr
 530 535 540
 Arg Ala Thr Val Pro Phe Pro Phe Asp Ile Lys Thr Leu Ile Ile Ala
 545 550 555 560
 Thr Thr Met Gly Phe Ile Ser Phe Leu Gly Val Val Leu Phe Cys Leu
 565 570 575
 Val Leu Leu Phe Leu Trp Ser Arg Gly Lys Gly Asn Thr Lys His Asn

580 585 590
 Ile Glu Ile Glu Tyr Val Pro Arg Lys Ser Asp Ala Gly Ile Ser Ser
 595 600 605

Ala Asp Ala Pro Arg Lys Phe Asn Met Lys Met Ile
 610 615 620

<210> 74

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 74

tcacctggag cctttattgg cc

22

<210> 75

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 75

ataccagcta taaccaggct gcg

23

<210> 76

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 76

caacagtaag tggtttgatg ctcttccaaa tctagagatt ctgatgattg
 gg

50

52

<210> 77

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 77
 ccatgtgtct cctcctacaa ag 22

<210> 78
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 78
 gggaatagat gtgatctgat tgg 23

<210> 79
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 79
 cacctgtagc aatgcaaadc tcaaggaaat acctagagat cttcctcctg 50

<210> 80
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 80
 agcaaccgcc tgaagctcat cc 22

<210> 81
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 81
 aaggcgcggt gaaagatgta gacg 24

<210> 82

<211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 82
 gactacatgt ttcaggacct gtacaacctc aagtcactgg aggttggcga 50

<210> 83
 <211> 1685
 <212> DNA
 <213> Homo sapiens

<400> 83
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 agccaggag cggccggga agcgcgatgg gggcccagc cgcctcgctc ctgctcctgc 180
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 ttggggagaa gagagccctt cgagataatc gaattcagct gggtacctct acgccccacg 420
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 tccacggaga accaaccgcg atacaggaag atcccaatgg taaaaccttc actgtcagca 720
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 aaaca 1685

<210> 84
 <211> 398
 <212> PRT
 <213> Homo sapiens

<400> 84

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 Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp Ser Asn
 50 55 60
 Pro Ala Gln Gln Thr Leu Tyr Phe Gly Glu Lys Arg Ala Leu Arg Asp
 65 70 75 80
 Asn Arg Ile Gln Leu Val Thr Ser Thr Pro His Glu Leu Ser Ile Ser
 85 90 95
 Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys Ser Ile
 100 105 110
 Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu Val Thr Val Leu Gly
 115 120 125
 Ile Pro Gln Lys Pro Ile Ile Thr Gly Tyr Lys Ser Ser Leu Arg Glu
 130 135 140
 Lys Asp Thr Ala Thr Leu Asn Cys Gln Ser Ser Gly Ser Lys Pro Ala
 145 150 155 160
 Ala Arg Leu Thr Trp Arg Lys Gly Asp Gln Glu Leu His Gly Glu Pro
 165 170 175
 Thr Arg Ile Gln Glu Asp Pro Asn Gly Lys Thr Phe Thr Val Ser Ser
 180 185 190
 Ser Val Thr Phe Gln Val Thr Arg Glu Asp Asp Gly Ala Ser Ile Val
 195 200 205
 Cys Ser Val Asn His Glu Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser
 210 215 220
 Gln Arg Ile Glu Val Leu Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp
 225 230 235 240
 Pro Pro His Pro Arg Glu Gly Gln Lys Leu Leu Leu His Cys Glu Gly
 245 250 255
 Arg Gly Asn Pro Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu Gly Ser
 260 265 270
 Val Pro Pro Leu Lys Met Thr Gln Glu Ser Ala Leu Ile Phe Pro Phe
 275 280 285

Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn
 290 295 300

Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser
 305 310 315 320

Pro Val Pro Ser Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile
 325 330 335

Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe Leu Gly
 340 345 350

His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys
 355 360 365

Gly Ser Asp Asp Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu
 370 375 380

Gly Gly Gln Ser Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile
 385 390 395

<210> 85

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 85

gctaggaatt ccacagaagc cc

22

<210> 86

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 86

aacctggaat gtcaccgagc tg

22

<210> 87

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

<400> 87
cctagcacag tgacgaggga cttggc 26

<210> 88
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 88
aagacacagc caccctaaac tgtcagtctt ctgggagcaa gcctgcagcc 50

<210> 89
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 89
gccctggcag acgagggcga gtacacctgc tcaatcttca ctatgcctgt 50

<210> 90
<211> 2755
<212> DNA
<213> Homo sapiens

<400> 90
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<210> 91
<211> 696
<212> PRT
<213> Homo sapiens
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Met Leu Leu Trp Ile Leu Leu Leu Glu Thr Ser Leu Cys Phe Ala Ala
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Gly Asn Val Thr Gly Asp Val Cys Lys Glu Lys Ile Cys Ser Cys Asn
20 25 30

Glu Ile Glu Gly Asp Leu His Val Asp Cys Glu Lys Lys Gly Phe Thr
35 40 45

Ser Leu Gln Arg Phe Thr Ala Pro Thr Ser Gln Phe Tyr His Leu Phe
50 55 60

Leu His Gly Asn Ser Leu Thr Arg Leu Phe Pro Asn Glu Phe Ala Asn
65 70 75 80

Phe Tyr Asn Ala Val Ser Leu His Met Glu Asn Asn Gly Leu His Glu
85 90 95

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Val | Pro | Gly | Ala | Phe | Leu | Gly | Leu | Gln | Leu | Val | Lys | Arg | Leu | His | 100 | 105 | 110 | |
| Ile | Asn | Asn | Asn | Lys | Ile | Lys | Ser | Phe | Arg | Lys | Gln | Thr | Phe | Leu | Gly | 115 | 120 | 125 | |
| Leu | Asp | Asp | Leu | Glu | Tyr | Leu | Gln | Ala | Asp | Phe | Asn | Leu | Leu | Arg | Asp | 130 | 135 | 140 | |
| Ile | Asp | Pro | Gly | Ala | Phe | Gln | Asp | Leu | Asn | Lys | Leu | Glu | Val | Leu | Ile | 145 | 150 | 155 | 160 |
| Leu | Asn | Asp | Asn | Leu | Ile | Ser | Thr | Leu | Pro | Ala | Asn | Val | Phe | Gln | Tyr | 165 | 170 | 175 | |
| Val | Pro | Ile | Thr | His | Leu | Asp | Leu | Arg | Gly | Asn | Arg | Leu | Lys | Thr | Leu | 180 | 185 | 190 | |
| Pro | Tyr | Glu | Glu | Val | Leu | Glu | Gln | Ile | Pro | Gly | Ile | Ala | Glu | Ile | Leu | 195 | 200 | 205 | |
| Leu | Glu | Asp | Asn | Pro | Trp | Asp | Cys | Thr | Cys | Asp | Leu | Leu | Ser | Leu | Lys | 210 | 215 | 220 | |
| Glu | Trp | Leu | Glu | Asn | Ile | Pro | Lys | Asn | Ala | Leu | Ile | Gly | Arg | Val | Val | 225 | 230 | 235 | 240 |
| Cys | Glu | Ala | Pro | Thr | Arg | Leu | Gln | Gly | Lys | Asp | Leu | Asn | Glu | Thr | Thr | 245 | 250 | 255 | |
| Glu | Gln | Asp | Leu | Cys | Pro | Leu | Lys | Asn | Arg | Val | Asp | Ser | Ser | Leu | Pro | 260 | 265 | 270 | |
| Ala | Pro | Pro | Ala | Gln | Glu | Glu | Thr | Phe | Ala | Pro | Gly | Pro | Leu | Pro | Thr | 275 | 280 | 285 | |
| Pro | Phe | Lys | Thr | Asn | Gly | Gln | Glu | Asp | His | Ala | Thr | Pro | Gly | Ser | Ala | 290 | 295 | 300 | |
| Pro | Asn | Gly | Gly | Thr | Lys | Ile | Pro | Gly | Asn | Trp | Gln | Ile | Lys | Ile | Arg | 305 | 310 | 315 | 320 |
| Pro | Thr | Ala | Ala | Ile | Ala | Thr | Gly | Ser | Ser | Arg | Asn | Lys | Pro | Leu | Ala | 325 | 330 | 335 | |
| Asn | Ser | Leu | Pro | Cys | Pro | Gly | Gly | Cys | Ser | Cys | Asp | His | Ile | Pro | Gly | 340 | 345 | 350 | |
| Ser | Gly | Leu | Lys | Met | Asn | Cys | Asn | Asn | Arg | Asn | Val | Ser | Ser | Leu | Ala | 355 | 360 | 365 | |
| Asp | Leu | Lys | Pro | Lys | Leu | Ser | Asn | Val | Gln | Glu | Leu | Phe | Leu | Arg | Asp | 370 | 375 | 380 | |

Asn Lys Ile His Ser Ile Arg Lys Ser His Phe Val Asp Tyr Lys Asn
 385 390 395 400
 Leu Ile Leu Leu Asp Leu Gly Asn Asn Asn Ile Ala Thr Val Glu Asn
 405 410 415
 Asn Thr Phe Lys Asn Leu Leu Asp Leu Arg Trp Leu Tyr Met Asp Ser
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 Asn Tyr Leu Asp Thr Leu Ser Arg Glu Lys Phe Ala Gly Leu Gln Asn
 435 440 445
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 Gly Thr Phe Asn Ala Met Pro Lys Leu Arg Ile Leu Ile Leu Asn Asn
 465 470 475 480
 Asn Leu Leu Arg Ser Leu Pro Val Asp Val Phe Ala Gly Val Ser Leu
 485 490 495
 Ser Lys Leu Ser Leu His Asn Asn Tyr Phe Met Tyr Leu Pro Val Ala
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 Gly Val Leu Asp Gln Leu Thr Ser Ile Ile Gln Ile Asp Leu His Gly
 515 520 525
 Asn Pro Trp Glu Cys Ser Cys Thr Ile Val Pro Phe Lys Gln Trp Ala
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 Glu Arg Leu Gly Ser Glu Val Leu Met Ser Asp Leu Lys Cys Glu Thr
 545 550 555 560
 Pro Val Asn Phe Phe Arg Lys Asp Phe Met Leu Leu Ser Asn Asp Glu
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 Ile Cys Pro Gln Leu Tyr Ala Arg Ile Ser Pro Thr Leu Thr Ser His
 580 585 590
 Ser Lys Asn Ser Thr Gly Leu Ala Glu Thr Gly Thr His Ser Asn Ser
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 Tyr Leu Asp Thr Ser Arg Val Ser Ile Ser Val Leu Val Pro Gly Leu
 610 615 620
 Leu Leu Val Phe Val Thr Ser Ala Phe Thr Val Val Gly Met Leu Val
 625 630 635 640
 Phe Ile Leu Arg Asn Arg Lys Arg Ser Lys Arg Arg Asp Ala Asn Ser
 645 650 655
 Ser Ala Ser Glu Ile Asn Ser Leu Gln Thr Val Cys Asp Ser Ser Tyr

660 665 670

Trp His Asn Gly Pro Tyr Asn Ala Asp Gly Ala His Arg Val Tyr Asp
675 680 685

Cys Gly Ser His Ser Leu Ser Asp
690 695

<210> 92
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 92
gttggatctg ggcaacaata ac 22

<210> 93
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 93
attgttgtgc aggctgagtt taag 24

<210> 94
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 94
ggtggctata catggatagc aattacctgg acacgctgtc ccggg 45

<210> 95
<211> 2226
<212> DNA
<213> Homo sapiens

<400> 95
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gctgcaccgg gcctggcagc gctccgcaca catttcctgt cgcggcctaa gggaaactgt 120
tggccgctgg gcccgcgggg ggattcttgg cagttggggg gtccgtcggg agcgagggcg 180

gaggggaagg gagggggaac cgggttgggg aagccagctg tagagggcgg tgaccgcgct 240
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<210> 96

<211> 490

<212> PRT

<213> Homo sapiens

<400> 96

Met Arg Pro Ala Phe Ala Leu Cys Leu Leu Trp Gln Ala Leu Trp Pro
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Gly Pro Gly Gly Gly Glu His Pro Thr Ala Asp Arg Ala Gly Cys Ser
 20 25 30

Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln
 35 40 45

Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val
 50 55 60

| | | | | | | | | | | | | | | | |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----------|
| Arg 65 | Ala | Gly | Ala | Glu | Leu | Arg | Ala | Val | Leu | Ala | Leu | Leu | Arg | Ala | Gly 80 |
| Pro | Gly | Pro | Gly | Gly | Gly | Ser | Lys | Asp | Leu | Leu | Phe | Trp | Val | Ala | Leu |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Glu | Arg | Arg | Arg | Ser | His | Cys | Thr | Leu | Glu | Asn | Glu | Pro | Leu | Arg | Gly |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Phe | Ser | Trp | Leu | Ser | Ser | Asp | Pro | Gly | Gly | Leu | Glu | Ser | Asp | Thr | Leu |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Gln | Trp | Val | Glu | Glu | Pro | Gln | Arg | Ser | Cys | Thr | Ala | Arg | Arg | Cys | Ala |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Val | Leu | Gln | Ala | Thr | Gly | Gly | Val | Glu | Pro | Ala | Gly | Trp | Lys | Glu | Met |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Arg | Cys | His | Leu | Arg | Ala | Asn | Gly | Tyr | Leu | Cys | Lys | Tyr | Gln | Phe | Glu |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Val | Leu | Cys | Pro | Ala | Pro | Arg | Pro | Gly | Ala | Ala | Ser | Asn | Leu | Ser | Tyr |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Arg | Ala | Pro | Phe | Gln | Leu | His | Ser | Ala | Ala | Leu | Asp | Phe | Ser | Pro | Pro |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Gly | Thr | Glu | Val | Ser | Ala | Leu | Cys | Arg | Gly | Gln | Leu | Pro | Ile | Ser | Val |
| | 210 | | | | 215 | | | | | 220 | | | | | |
| Thr | Cys | Ile | Ala | Asp | Glu | Ile | Gly | Ala | Arg | Trp | Asp | Lys | Leu | Ser | Gly |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Asp | Val | Leu | Cys | Pro | Cys | Pro | Gly | Arg | Tyr | Leu | Arg | Ala | Gly | Lys | Cys |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Ala | Glu | Leu | Pro | Asn | Cys | Leu | Asp | Asp | Leu | Gly | Gly | Phe | Ala | Cys | Glu |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Cys | Ala | Thr | Gly | Phe | Glu | Leu | Gly | Lys | Asp | Gly | Arg | Ser | Cys | Val | Thr |
| | | 275 | | | | | 280 | | | | | 285 | | | |
| Ser | Gly | Glu | Gly | Gln | Pro | Thr | Leu | Gly | Gly | Thr | Gly | Val | Pro | Thr | Arg |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Arg | Pro | Pro | Ala | Thr | Ala | Thr | Ser | Pro | Val | Pro | Gln | Arg | Thr | Trp | Pro |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| Ile | Arg | Val | Asp | Glu | Lys | Leu | Gly | Glu | Thr | Pro | Leu | Val | Pro | Glu | Gln |
| | | | | 325 | | | | | 330 | | | | | 335 | |
| Asp | Asn | Ser | Val | Thr | Ser | Ile | Pro | Glu | Ile | Pro | Arg | Trp | Gly | Ser | Glu |

| | | |
|---|-----|-----|
| 340 | 345 | 350 |
| Ser Thr Met Ser Thr Leu Gln Met Ser Leu Gln Ala Glu Ser Lys Ala | | |
| 355 | 360 | 365 |
| Thr Ile Thr Pro Ser Gly Ser Val Ile Ser Lys Phe Asn Ser Thr Thr | | |
| 370 | 375 | 380 |
| Ser Ser Ala Thr Pro Gln Ala Phe Asp Ser Ser Ser Ala Val Val Phe | | |
| 385 | 390 | 395 |
| Ile Phe Val Ser Thr Ala Val Val Val Leu Val Ile Leu Thr Met Thr | | |
| 405 | 410 | 415 |
| Val Leu Gly Leu Val Lys Leu Cys Phe His Glu Ser Pro Ser Ser Gln | | |
| 420 | 425 | 430 |
| Pro Arg Lys Glu Ser Met Gly Pro Pro Gly Leu Glu Ser Asp Pro Glu | | |
| 435 | 440 | 445 |
| Pro Ala Ala Leu Gly Ser Ser Ser Ala His Cys Thr Asn Asn Gly Val | | |
| 450 | 455 | 460 |
| Lys Val Gly Asp Cys Asp Leu Arg Asp Arg Ala Glu Gly Ala Leu Leu | | |
| 465 | 470 | 475 |
| Ala Glu Ser Pro Leu Gly Ser Ser Asp Ala | | |
| 485 | 490 | |

<210> 97

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 97

tggaaggaga tgcgatgccca cctg

24

<210> 98

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 98

tgaccagtgg ggaaggacag

20

<210> 99
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 99
 acagagcaga gggcgccttg 20

 <210> 100
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 100
 tcagggacaa gtggtgtctc tccc 24

 <210> 101
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 101
 tcagggaagg agtgtgcagt tctg 24

 <210> 102
 <211> 50
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 102
 acagctcccc atctcagtta cttgcatcgc ggacgaaatc ggcgcctcgt 50

 <210> 103
 <211> 2026
 <212> DNA
 <213> Homo sapiens

<400> 103

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tatcccccg ctacctgggc cgcgccgcgc cggtgcgcg gtgagaggga gcgcgcgggc 180
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cagctctcgc ggcagcagtc cccagagaga cctgttttca catgtggtgg cattcttact 420
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gtgttatttg tttcaccttc aagcctttgc cctgaggtgt tacaatcttg tottgcgttt 1980
tctaaatcaa tgcttaataa aatattttta aaggaaaaaa aaaaaa 2026

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<210> 104

<211> 415

<212> PRT

<213> Homo sapiens

<400> 104

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Met Arg Gly Ala Asn Ala Trp Ala Pro Leu Cys Leu Leu Leu Ala Ala
  1                      5                      10                      15

Ala Thr Gln Leu Ser Arg Gln Gln Ser Pro Glu Arg Pro Val Phe Thr
                20                      25                      30

Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly
                35                      40                      45

Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr
    50                      55                      60

```

Val Pro Glu Gly Lys Val Val Val Leu Asn Phe Arg Phe Ile Asp Leu
 65 70 75 80
 Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe Val Asp Val Tyr Asn Gly
 85 90 95
 His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro
 100 105 110
 Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser
 115 120 125
 Asp Ala Asn Thr Ala Gly Asn Gly Phe Met Ala Met Phe Ser Ala Ala
 130 135 140
 Glu Pro Asn Glu Arg Gly Asp Gln Tyr Cys Gly Gly Leu Leu Asp Arg
 145 150 155 160
 Pro Ser Gly Ser Phe Lys Thr Pro Asn Trp Pro Asp Arg Asp Tyr Pro
 165 170 175
 Ala Gly Val Thr Cys Val Trp His Ile Val Ala Pro Lys Asn Gln Leu
 180 185 190
 Ile Glu Leu Lys Phe Glu Lys Phe Asp Val Glu Arg Asp Asn Tyr Cys
 195 200 205
 Arg Tyr Asp Tyr Val Ala Val Phe Asn Gly Gly Glu Val Asn Asp Ala
 210 215 220
 Arg Arg Ile Gly Lys Tyr Cys Gly Asp Ser Pro Pro Ala Pro Ile Val
 225 230 235 240
 Ser Glu Arg Asn Glu Leu Leu Ile Gln Phe Leu Ser Asp Leu Ser Leu
 245 250 255
 Thr Ala Asp Gly Phe Ile Gly His Tyr Ile Phe Arg Pro Lys Lys Leu
 260 265 270
 Pro Thr Thr Thr Glu Gln Pro Val Thr Thr Thr Phe Pro Val Thr Thr
 275 280 285
 Gly Leu Lys Pro Thr Val Ala Leu Cys Gln Gln Lys Cys Arg Arg Thr
 290 295 300
 Gly Thr Leu Glu Gly Asn Tyr Cys Ser Ser Asp Phe Val Leu Ala Gly
 305 310 315 320
 Thr Val Ile Thr Thr Ile Thr Arg Asp Gly Ser Leu His Ala Thr Val
 325 330 335
 Ser Ile Ile Asn Ile Tyr Lys Glu Gly Asn Leu Ala Ile Gln Gln Ala

| | | |
|---|-------------------------------------|-----|
| 340 | 345 | 350 |
| Gly Lys Asn Met Ser Ala Arg | Leu Thr Val Val Cys Lys Gln Cys Pro | |
| 355 | 360 | 365 |
| Leu Leu Arg Arg Gly Leu Asn Tyr Ile Ile Met Gly Gln Val Gly Glu | | |
| 370 | 375 | 380 |
| Asp Gly Arg Gly Lys Ile Met Pro Asn Ser Phe Ile Met Met Phe Lys | | |
| 385 | 390 | 395 |
| Thr Lys Asn Gln Lys Leu Leu Asp Ala Leu Lys Asn Lys Gln Cys | | |
| 405 | 410 | 415 |

<210> 105

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 105

ccgattcata gacctcgaga gt

22

<210> 106

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 106

gtcaaggagt cctccacaat ac

22

<210> 107

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 107

gtgtacaatg gccatgccaa tggccagcgc attggccgct tctgt

45

<210> 108

<211> 1838

<212> DNA

<213> Homo sapiens

<400> 108

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aagggcctag tcccagctgt gctctggggc ctcagcctct tcctcaacct cccaggacct 180
atctggctcc agccctctcc acctccccag tcttctcccc cgcctcagcc ccatccgtgt 240
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ggtcttgtaa agttaaaaaa aaaaaaaaaa aaaaaaaa 1838

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<210> 109

<211> 420

<212> PRT

<213> Homo sapiens

<400> 109

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Met Ala Pro Trp Pro Pro Lys Gly Leu Val Pro Ala Val Leu Trp Gly
  1                      5                      10                      15

Leu Ser Leu Phe Leu Asn Leu Pro Gly Pro Ile Trp Leu Gln Pro Ser
      20                      25                      30

Pro Pro Pro Gln Ser Ser Pro Pro Pro Gln Pro His Pro Cys His Thr
      35                      40                      45

Cys Arg Gly Leu Val Asp Ser Phe Asn Lys Gly Leu Glu Arg Thr Ile
      50                      55                      60

```

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Asp | Asn | Phe | Gly | Gly | Gly | Asn | Thr | Ala | Trp | Glu | Glu | Glu | Asn | Leu | 65 | 70 | 75 | 80 |
| Ser | Lys | Tyr | Lys | Asp | Ser | Glu | Thr | Arg | Leu | Val | Glu | Val | Leu | Glu | Gly | 85 | 90 | 95 | |
| Val | Cys | Ser | Lys | Ser | Asp | Phe | Glu | Cys | His | Arg | Leu | Leu | Glu | Leu | Ser | 100 | 105 | 110 | |
| Glu | Glu | Leu | Val | Glu | Ser | Trp | Trp | Phe | His | Lys | Gln | Gln | Glu | Ala | Pro | 115 | 120 | 125 | |
| Asp | Leu | Phe | Gln | Trp | Leu | Cys | Ser | Asp | Ser | Leu | Lys | Leu | Cys | Cys | Pro | 130 | 135 | 140 | |
| Ala | Gly | Thr | Phe | Gly | Pro | Ser | Cys | Leu | Pro | Cys | Pro | Gly | Gly | Thr | Glu | 145 | 150 | 155 | 160 |
| Arg | Pro | Cys | Gly | Gly | Tyr | Gly | Gln | Cys | Glu | Gly | Glu | Gly | Thr | Arg | Gly | 165 | 170 | 175 | |
| Gly | Ser | Gly | His | Cys | Asp | Cys | Gln | Ala | Gly | Tyr | Gly | Gly | Glu | Ala | Cys | 180 | 185 | 190 | |
| Gly | Gln | Cys | Gly | Leu | Gly | Tyr | Phe | Glu | Ala | Glu | Arg | Asn | Ala | Ser | His | 195 | 200 | 205 | |
| Leu | Val | Cys | Ser | Ala | Cys | Phe | Gly | Pro | Cys | Ala | Arg | Cys | Ser | Gly | Pro | 210 | 215 | 220 | |
| Glu | Glu | Ser | Asn | Cys | Leu | Gln | Cys | Lys | Lys | Gly | Trp | Ala | Leu | His | His | 225 | 230 | 235 | 240 |
| Leu | Lys | Cys | Val | Asp | Ile | Asp | Glu | Cys | Gly | Thr | Glu | Gly | Ala | Asn | Cys | 245 | 250 | 255 | |
| Gly | Ala | Asp | Gln | Phe | Cys | Val | Asn | Thr | Glu | Gly | Ser | Tyr | Glu | Cys | Arg | 260 | 265 | 270 | |
| Asp | Cys | Ala | Lys | Ala | Cys | Leu | Gly | Cys | Met | Gly | Ala | Gly | Pro | Gly | Arg | 275 | 280 | 285 | |
| Cys | Lys | Lys | Cys | Ser | Pro | Gly | Tyr | Gln | Gln | Val | Gly | Ser | Lys | Cys | Leu | 290 | 295 | 300 | |
| Asp | Val | Asp | Glu | Cys | Glu | Thr | Glu | Val | Cys | Pro | Gly | Glu | Asn | Lys | Gln | 305 | 310 | 315 | 320 |
| Cys | Glu | Asn | Thr | Glu | Gly | Gly | Tyr | Arg | Cys | Ile | Cys | Ala | Glu | Gly | Tyr | 325 | 330 | 335 | |
| Lys | Gln | Met | Glu | Gly | Ile | Cys | Val | Lys | Glu | Gln | Ile | Pro | Glu | Ser | Ala | 340 | 345 | 350 | |

Gly Phe Phe Ser Glu Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln
 355 360 365

Met Phe Phe Gly Ile Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys
 370 375 380

Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met
 385 390 395 400

Thr Gly Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe
 405 410 415

Ile Lys Gly Arg
 420

<210> 110

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 110

cctggctatc agcaggtggg ctccaagtgt ctcgatgtgg atgagtgtga 50

<210> 111

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 111

attctgcgtg aacactgagg gc 22

<210> 112

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 112

atctgcttgt agccctcggc ac 22

<210> 113

<211> 1616
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (1461)
 <223> a, t, c or g

<400> 113
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<210> 114
 <211> 366
 <212> PRT
 <213> Homo sapiens

<400> 114
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 Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg Ala Asp Met
 35 40 45

Glu Glu Leu Val Ile Pro Thr His Val Arg Ala Gln Tyr Val Ala Leu
 50 55 60
 Leu Gln Arg Ser His Gly Asp Arg Ser Arg Gly Lys Arg Phe Ser Gln
 65 70 75 80
 Ser Phe Arg Glu Val Ala Gly Arg Phe Leu Ala Leu Glu Ala Ser Thr
 85 90 95
 His Leu Leu Val Phe Gly Met Glu Gln Arg Leu Pro Pro Asn Ser Glu
 100 105 110
 Leu Val Gln Ala Val Leu Arg Leu Phe Gln Glu Pro Val Pro Lys Ala
 115 120 125
 Ala Leu His Arg His Gly Arg Leu Ser Pro Arg Ser Ala Arg Ala Arg
 130 135 140
 Val Thr Val Glu Trp Leu Arg Val Arg Asp Asp Gly Ser Asn Arg Thr
 145 150 155 160
 Ser Leu Ile Asp Ser Arg Leu Val Ser Val His Glu Ser Gly Trp Lys
 165 170 175
 Ala Phe Asp Val Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg
 180 185 190
 Pro Arg Gln Pro Leu Leu Leu Gln Val Ser Val Gln Arg Glu His Leu
 195 200 205
 Gly Pro Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln
 210 215 220
 Gly Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu
 225 230 235 240
 Asp Leu Gly Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala Pro
 245 250 255
 Met Thr Glu Gly Thr Arg Cys Cys Arg Gln Glu Met Tyr Ile Asp Leu
 260 265 270
 Gln Gly Met Lys Trp Ala Glu Asn Trp Val Leu Glu Pro Pro Gly Phe
 275 280 285
 Leu Ala Tyr Glu Cys Val Gly Thr Cys Arg Gln Pro Pro Glu Ala Leu
 290 295 300
 Ala Phe Lys Trp Pro Phe Leu Gly Pro Arg Gln Cys Ile Ala Ser Glu
 305 310 315 320
 Thr Asp Ser Leu Pro Met Ile Val Ser Ile Lys Glu Gly Gly Arg Thr
 325 330 335

Arg Pro Gln Val Val Ser Leu Pro Asn Met Arg Val Gln Lys Cys Ser
 340 345 350

Cys Ala Ser Asp Gly Ala Leu Val Pro Arg Arg Leu Gln Pro
 355 360 365

<210> 115

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 115

aggactgccca taacttgcct g 21

<210> 116

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 116

ataggagttg aagcagcgct gc 22

<210> 117

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 117

tgtgtggaca tagacgagtg ccgctaccgc tactgccagc accgc 45

<210> 118

<211> 1857

<212> DNA

<213> Homo sapiens

<400> 118

gtctgttccc aggagtcctt cggcggctgt tgtgtcagtg gcctgacgc gatggggaca 60
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 ctggcattgg gcagtgttac agtgcactct tctgaacctg aagtcagaat tcctgagaat 180

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<210> 119

<211> 299

<212> PRT

<213> Homo sapiens

<400> 119

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Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His
20 25 30

Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu
35 40 45

Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe
50 55 60

Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr
65 70 75 80

Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe
85 90 95

Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser
 100 105 110
 Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val
 115 120 125
 Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr
 130 135 140
 Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro
 145 150 155 160
 Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn
 165 170 175
 Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro
 180 185 190
 Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly
 195 200 205
 Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser
 210 215 220
 Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val
 225 230 235 240
 Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly
 245 250 255
 Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly
 260 265 270
 Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu
 275 280 285
 Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val
 290 295

<210> 120

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 120

tcgcggagct gtgttctgtt tccc

24

<210> 121

<211> 50

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 121
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 <210> 122
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 122
 acacctgggtt caaagatggg 20

 <210> 123
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 123
 taggaagagt tgctgaaggc acgg 24

 <210> 124
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 124
 ttgccttact caggtgctac 20

 <210> 125
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

<400> 125
actcagcagt ggtaggaaag 20

<210> 126
<211> 1210
<212> DNA
<213> Homo sapiens

<400> 126
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<210> 127
<211> 282
<212> PRT
<213> Homo sapiens

<400> 127
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35 40 45
Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser
50 55 60
Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys
65 70 75 80

Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg Ile Glu Pro Cys Thr Gln
 85 90 95
 Lys Gly Gln Cys Pro Pro Pro Pro Gly Leu Pro Cys Pro Cys Thr Gly
 100 105 110
 Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Lys Leu Arg Asn Cys Ser
 115 120 125
 Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu Ser Asp Asp
 130 135 140
 Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp Cys Pro Asp
 145 150 155 160
 Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly
 165 170 175
 Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser
 180 185 190
 Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val
 195 200 205
 Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly
 210 215 220
 Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Ala Val Leu Ser Ala
 225 230 235 240
 Ser Leu Val Thr Ala Thr Leu Leu Leu Leu Ser Trp Leu Arg Ala Gln
 245 250 255
 Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu Ser Leu
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 Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro
 275 280

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 128

aagttccagt gccgcaccag tggc

24

<210> 129

<211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 129
 ttggttccac agccgagctc gtcg 24

<210> 130
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 130
 gaggaggagt gcaggattga gccatgtacc cagaaagggc aatgcccacc 50

<210> 131
 <211> 1843
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (1837)
 <223> a, t, c or g

<400> 131
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<210> 132

<211> 490

<212> PRT

<213> Homo sapiens

<400> 132

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          20           25           30

Ile Leu Trp Phe Gln Leu Ala Leu Cys Phe Gly Pro Ala Gln Leu Thr
    35           40           45

Gly Gly Phe Asp Asp Leu Gln Val Cys Ala Asp Pro Gly Ile Pro Glu
    50           55           60

Asn Gly Phe Arg Thr Pro Ser Gly Gly Val Phe Phe Glu Gly Ser Val
    65           70           75           80

Ala Arg Phe His Cys Gln Asp Gly Phe Lys Leu Lys Gly Ala Thr Lys
          85           90           95

Arg Leu Cys Leu Lys His Phe Asn Gly Thr Leu Gly Trp Ile Pro Ser
    100           105           110

Asp Asn Ser Ile Cys Val Gln Glu Asp Cys Arg Ile Pro Gln Ile Glu
    115           120           125

Asp Ala Glu Ile His Asn Lys Thr Tyr Arg His Gly Glu Lys Leu Ile
    130           135           140

Ile Thr Cys His Glu Gly Phe Lys Ile Arg Tyr Pro Asp Leu His Asn
    145           150           155           160

Met Val Ser Leu Cys Arg Asp Asp Gly Thr Trp Asn Asn Leu Pro Ile
          165           170           175

Cys Gln Gly Cys Leu Arg Pro Leu Ala Ser Ser Asn Gly Tyr Val Asn

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ile | Ser | Glu | Leu | Gln | Thr | Ser | Phe | Pro | Val | Gly | Thr | Val | Ile | Ser | Tyr | |
| 195 | | | | | 200 | | | | | 205 | | | | | | |
| Arg | Cys | Phe | Pro | Gly | Phe | Lys | Leu | Asp | Gly | Ser | Ala | Tyr | Leu | Glu | Cys | |
| 210 | | | | | 215 | | | | | 220 | | | | | | |
| Leu | Gln | Asn | Leu | Ile | Trp | Ser | Ser | Ser | Pro | Pro | Arg | Cys | Leu | Ala | Leu | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| Glu | Ala | Gln | Val | Cys | Pro | Leu | Pro | Pro | Met | Val | Ser | His | Gly | Asp | Phe | |
| 245 | | | | | 250 | | | | | 255 | | | | | | |
| Val | Cys | His | Pro | Arg | Pro | Cys | Glu | Arg | Tyr | Asn | His | Gly | Thr | Val | Val | |
| 260 | | | | | 265 | | | | | 270 | | | | | | |
| Glu | Phe | Tyr | Cys | Asp | Pro | Gly | Tyr | Ser | Leu | Thr | Ser | Asp | Tyr | Lys | Tyr | |
| 275 | | | | | 280 | | | | | 285 | | | | | | |
| Ile | Thr | Cys | Gln | Tyr | Gly | Glu | Trp | Phe | Pro | Ser | Tyr | Gln | Val | Tyr | Cys | |
| 290 | | | | | 295 | | | | | 300 | | | | | | |
| Ile | Lys | Ser | Glu | Gln | Thr | Trp | Pro | Ser | Thr | His | Glu | Thr | Leu | Leu | Thr | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| Thr | Trp | Lys | Ile | Val | Ala | Phe | Thr | Ala | Thr | Ser | Val | Leu | Leu | Val | Leu | |
| 325 | | | | | 330 | | | | | 335 | | | | | | |
| Leu | Leu | Val | Ile | Leu | Ala | Arg | Met | Phe | Gln | Thr | Lys | Phe | Lys | Ala | His | |
| 340 | | | | | 345 | | | | | 350 | | | | | | |
| Phe | Pro | Pro | Arg | Gly | Pro | Pro | Arg | Ser | Ser | Ser | Ser | Asp | Pro | Asp | Phe | |
| 355 | | | | | 360 | | | | | 365 | | | | | | |
| Val | Val | Val | Asp | Gly | Val | Pro | Val | Met | Leu | Pro | Ser | Tyr | Asp | Glu | Ala | |
| 370 | | | | | 375 | | | | | 380 | | | | | | |
| Val | Ser | Gly | Gly | Leu | Ser | Ala | Leu | Gly | Pro | Gly | Tyr | Met | Ala | Ser | Val | |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 | |
| Gly | Gln | Gly | Cys | Pro | Leu | Pro | Val | Asp | Asp | Gln | Ser | Pro | Pro | Ala | Tyr | |
| 405 | | | | | 410 | | | | | 415 | | | | | | |
| Pro | Gly | Ser | Gly | Asp | Thr | Asp | Thr | Gly | Pro | Gly | Glu | Ser | Glu | Thr | Cys | |
| 420 | | | | | 425 | | | | | 430 | | | | | | |
| Asp | Ser | Val | Ser | Gly | Ser | Ser | Glu | Leu | Leu | Gln | Ser | Leu | Tyr | Ser | Pro | |
| 435 | | | | | 440 | | | | | 445 | | | | | | |
| Pro | Arg | Cys | Gln | Glu | Ser | Thr | His | Pro | Ala | Ser | Asp | Asn | Pro | Asp | Ile | |
| 450 | | | | | 455 | | | | | 460 | | | | | | |

Ile Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His
 465 470 475 480

His Ala His Trp Val Leu Phe Leu Arg Asn
 485 490

<210> 133

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 133

atctcctatc gctgctttcc cgg 23

<210> 134

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 134

agccaggatc gcagtaaaac tcc 23

<210> 135

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 135

atttaaactt gatgggtctg cgtatcttga gtgcttaca aaccttatct 50

<210> 136

<211> 1815

<212> DNA

<213> Homo sapiens

<400> 136

cccacgcgtc cgctccgcgc cctccccccc gcctcccgctg cggtcgctcg gtggcctaga 60
 gatgctgctg ccgcggttgc agttgtcgcg cagcctctg cccgccagcc cgctccaccg 120
 ccgtagcgcc cgagtgtcgg ggggcgcacc cgagtcgggc catgaggccg ggaaccgcgc 180
 tacaggcgt gctgctggcc gtgctgctgg tggggctgcg ggccgcgaac ggctgcctgc 240
 tgagtgcctc ggatttgac ctcagaggag ggcagccagt ctgccgggga gggacacaga 300

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ggccttgтта taaagtcatt tacttccatg atactttctcg aagactgaac tttgaggaag 360
ccaaagaagc ctgcaggagg gatggaggcc agctagtcag catcgagtct gaagatgaac 420
agaaactgat agaaaagttc attgaaaacc tcttgccatc tgatggtgac ttctggattg 480
ggctcaggag gcgtgaggag aaacaaagca atagcacagc ctgccaggac ctttatgctt 540
ggactgatgg cagcatatca caatttagga actggtatgt ggatgagccg tcctgcggca 600
gcgagggtctg cgtgggtcatg taccatcagc catcggcacc cgctggcatc ggaggcccct 660
acatgtttcca gtggaatgat gaccggtgca acatgaagaa caatttcatt tgcaaatatt 720
ctgatgagaa accagcagtt ccttctagag aagctgaagg tgaggaaaca gagctgacaa 780
cacctgtact tccagaagaa acacaggaag aagatgccaa aaaaacattt aaagaaagta 840
gagaagctgc cttgaatctg gcctacatcc taatccccag cattccccctt ctctctctcc 900
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cagaccctag cacaaagaag caacacacca tctggccctc tcctcaccag ggaaacagcc 1020
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tgagcgtgga gagtggattt gtgaccaatg acatttatga gttctcccca gaccaaattg 1260
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tccagctcga cttatgaga aggtaccttg cccaggctctg gcacatagta gagtctcaat 1560
aaatgtcact tggttggttg tatctaactt ttaagggaca gagctttacc tggcagtgat 1620
aaagatgggc tgtggagctt ggaaaaccac ctctgttttc cttgctctat acagcagcac 1680
atattatcat acagacagaa aatccagaat cttttcaaag cccacatatg gtagcacagg 1740
ttggcctgtg catcggaat tctcatatct gtttttttca aagaataaaa tcaaataaag 1800
agcaggaaaa aaaaa 1815

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<210> 137

<211> 382

<212> PRT

<213> Homo sapiens

<400> 137

```

Met Arg Pro Gly Thr Ala Leu Gln Ala Val Leu Leu Ala Val Leu Leu
  1             5             10             15

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```

Val Gly Leu Arg Ala Ala Thr Gly Arg Leu Leu Ser Ala Ser Asp Leu
      20             25             30

```

```

Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro
      35             40             45

```

```

Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg Leu Asn Phe
      50             55             60

```

```

Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gly Gln Leu Val Ser
      65             70             75             80

```

```

Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe Ile Glu Asn
      85             90             95

```

```

Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Arg Glu
      100            105            110

```

Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr Ala Trp Thr
 115 120 125
 Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser
 130 135 140
 Cys Gly Ser Glu Val Cys Val Val Met Tyr His Gln Pro Ser Ala Pro
 145 150 155 160
 Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys
 165 170 175
 Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala
 180 185 190
 Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro
 195 200 205
 Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys
 210 215 220
 Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser
 225 230 235 240
 Ile Pro Leu Leu Leu Leu Leu Val Val Thr Thr Val Val Cys Trp Val
 245 250 255
 Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys
 260 265 270
 Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn Ser Pro Asp
 275 280 285
 Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu Ala Asp Leu Ala
 290 295 300
 Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe Arg Val Cys Ser Gly
 305 310 315 320
 Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr Asp Asn Met Ala Val
 325 330 335
 Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val Ser Val Glu Ser Gly
 340 345 350
 Phe Val Thr Asn Asp Ile Tyr Glu Phe Ser Pro Asp Gln Met Gly Arg
 355 360 365
 Ser Lys Glu Ser Gly Trp Val Glu Asn Glu Ile Tyr Gly Tyr
 370 375 380

<210> 138

<211> 50
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 138
 gttcattgaa aacctcttgc catctgatgg tgacttctgg attgggctca 50

 <210> 139
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 139
 aagccaaaga agcctgcagg aggg 24

 <210> 140
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 140
 cagtccaagc ataaaggtcc tggc 24

 <210> 141
 <211> 1514
 <212> DNA
 <213> Homo sapiens

 <400> 141
 ggggtctccc tcagggccgg gaggcacagc ggtccctgct tgctgaaggg ctggatgtac 60
 gcatccgcag gttcccgcgg acttgggggc gcccgctgag ccccggcgcc cgcagaagac 120
 ttgtgtttgc ctctgcagc ctcaaccggg agggcagcga gggcctacca ccatgatcac 180
 tgggtgtgttc agcatgcgct tgtggacccc agtggcgctc ctgacctcgc tggcgctactg 240
 cctgcaccag cggcggggtg ccttgccgga gctgcaggag gccgatggcc agtgtccggt 300
 cgaccgcagc ctgctgaagt tgaaaatggt gcaggctcgtg ttctgacacg gggctcggag 360
 tcctctcaag ccgctcccgc tggaggagca ggtagagtgg aacccccagc tattagaggt 420
 cccaccccaa actcagtttg attacacagt caccaatcta gctggtggtc cgaaaccata 480
 ttctccttac gactctcaat accatgagac caccctgaag gggggcatgt ttgctgggca 540
 gctgaccaag gtgggcatgc agcaaatgtt tgccttggga gagagactga ggaagaacta 600
 tgtggaagac attccctttc tttcaccaac cttcaaccca caggaggtct ttattcgttc 660
 cactaacatt ttctggaatc tggagtccac ccgttgtttg ctggctgggc ttttccagtg 720

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tcagaaagaa ggacccatca tcatccacac tgatgaagca gattcagaag tcttgtatcc 780
caactaccaa agctgctgga gcctgaggca gagaaccaga ggccggaggc agactgcctc 840
tttacagcca ggaatctcag aggatttgaa aaagggtgaag gacaggatgg gcattgacag 900
tagtgataaa gtggacttct tcatcctcct ggacaacgtg gctgccgagc aggcacacaa 960
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caagatcaga aagctgtatc tctatgcggc tcatgatgtg accttcatac cgtctttaat 1200
gaccctgggg atttttgacc acaaatggcc accgtttgct gttgacctga ccatggaact 1260
ttaccagcac ctggaatcta aggagtgggt tgtgcagctc tattaccacg ggaaggagca 1320
ggtgccgaga ggttgccctg atgggctctg cccgctggac atgttcttga atgccatgtc 1380
agttttatac ttaagcccag aaaaatacca tgcactctgc tctcaaactc aggtgatgga 1440
agttggaaat gaagagtaac tgatttataa aagcaggatg tgttgatttt aaaataaagt 1500
gcctttatac aatg 1514

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<210> 142

<211> 428

<212> PRT

<213> Homo sapiens

<400> 142

```

Met Ile Thr Gly Val Phe Ser Met Arg Leu Trp Thr Pro Val Gly Val
  1             5             10             15

```

```

Leu Thr Ser Leu Ala Tyr Cys Leu His Gln Arg Arg Val Ala Leu Ala
      20             25             30

```

```

Glu Leu Gln Glu Ala Asp Gly Gln Cys Pro Val Asp Arg Ser Leu Leu
      35             40             45

```

```

Lys Leu Lys Met Val Gln Val Val Phe Arg His Gly Ala Arg Ser Pro
      50             55             60

```

```

Leu Lys Pro Leu Pro Leu Glu Glu Gln Val Glu Trp Asn Pro Gln Leu
      65             70             75             80

```

```

Leu Glu Val Pro Pro Gln Thr Gln Phe Asp Tyr Thr Val Thr Asn Leu
      85             90             95

```

```

Ala Gly Gly Pro Lys Pro Tyr Ser Pro Tyr Asp Ser Gln Tyr His Glu
      100            105            110

```

```

Thr Thr Leu Lys Gly Gly Met Phe Ala Gly Gln Leu Thr Lys Val Gly
      115            120            125

```

```

Met Gln Gln Met Phe Ala Leu Gly Glu Arg Leu Arg Lys Asn Tyr Val
      130            135            140

```

```

Glu Asp Ile Pro Phe Leu Ser Pro Thr Phe Asn Pro Gln Glu Val Phe
      145            150            155            160

```

```

Ile Arg Ser Thr Asn Ile Phe Arg Asn Leu Glu Ser Thr Arg Cys Leu
      165            170            175

```

Leu Ala Gly Leu Phe Gln Cys Gln Lys Glu Gly Pro Ile Ile Ile His
 180 185 190
 Thr Asp Glu Ala Asp Ser Glu Val Leu Tyr Pro Asn Tyr Gln Ser Cys
 195 200 205
 Trp Ser Leu Arg Gln Arg Thr Arg Gly Arg Arg Gln Thr Ala Ser Leu
 210 215 220
 Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg Met Gly
 225 230 235 240
 Ile Asp Ser Ser Asp Lys Val Asp Phe Phe Ile Leu Leu Asp Asn Val
 245 250 255
 Ala Ala Glu Gln Ala His Asn Leu Pro Ser Cys Pro Met Leu Lys Arg
 260 265 270
 Phe Ala Arg Met Ile Glu Gln Arg Ala Val Asp Thr Ser Leu Tyr Ile
 275 280 285
 Leu Pro Lys Glu Asp Arg Glu Ser Leu Gln Met Ala Val Gly Pro Phe
 290 295 300
 Leu His Ile Leu Glu Ser Asn Leu Leu Lys Ala Met Asp Ser Ala Thr
 305 310 315 320
 Ala Pro Asp Lys Ile Arg Lys Leu Tyr Leu Tyr Ala Ala His Asp Val
 325 330 335
 Thr Phe Ile Pro Leu Leu Met Thr Leu Gly Ile Phe Asp His Lys Trp
 340 345 350
 Pro Pro Phe Ala Val Asp Leu Thr Met Glu Leu Tyr Gln His Leu Glu
 355 360 365
 Ser Lys Glu Trp Phe Val Gln Leu Tyr Tyr His Gly Lys Glu Gln Val
 370 375 380
 Pro Arg Gly Cys Pro Asp Gly Leu Cys Pro Leu Asp Met Phe Leu Asn
 385 390 395 400
 Ala Met Ser Val Tyr Thr Leu Ser Pro Glu Lys Tyr His Ala Leu Cys
 405 410 415
 Ser Gln Thr Gln Val Met Glu Val Gly Asn Glu Glu
 420 425

<210> 143

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 143

ccaactacca aagctgctgg agcc

24

<210> 144

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 144

gcagctctat taccacggga agga

24

<210> 145

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 145

tccttcccgt ggtaatagag ctgc

24

<210> 146

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 146

ggcagagaac cagaggccgg aggagactgc ctctttacag ccagg

45

<210> 147

<211> 1686

<212> DNA

<213> Homo sapiens

<400> 147

ctcctcttaa cataacttgca gctaaaacta aatattgctg cttggggacc tccttctagc 60
cttaaatttc agctcatcac cttcacctgc cttggtcacg gctctgctat tctccttgat 120
ccttgccatt tgcaccagac ctggattcct agcgtctcca tctggagtgc ggctgggtggg 180

gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt ggggcaccgt 240
 gtgtgatgac ggctgggaca ttaaggacgt ggctgtgttg tgccgggagc tgggctgtgg 300
 agctgccagc ggaacccta gtggtatatt gtatgagcca ccagcagaaa aagagcaaaa 360
 ggtcctcatc caatcagtca gttgcacagg aacagaagat acattggctc agtgtgagca 420
 agaagaagtt tatgattggt cacatgatga agatgctggg gcatcgtgtg agaaccaga 480
 gagctctttc tcccaggtcc cagaggggtg caggctggct gacggccctg ggcattgcaa 540
 gggacgcgtg gaagtgaagc accagaacca gtggtatacc gtgtgccaga caggctggag 600
 cctccggggc gcaaagggtg tgtgccggca gctgggatgt gggagggctg tactgactca 660
 aaaacgctgc aacaagcatg cctatggccg aaaacccatc tggctgagcc agatgtcatg 720
 ctccaggacg gaagcaaccc ttcaggattg cccttctggg ccttggggga agaacacctg 780
 caaccatgat gaagacacgt gggtcgaatg tgaagatccc tttgacttga gactagtagg 840
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 tgtttctctg aagaactctg acaaaatata gattttggta ctgaaagaga ttctagagga 1560
 acggaatttt aaggataaat tttctgaatt gggttatggg tttctgaaat tggctctata 1620
 atctaattag atataaaaatt ctggtaactt tatttacaat aataaagata gcactatgtg 1680
 ttcaaa 1686

<210> 148

<211> 347

<212> PRT

<213> Homo sapiens

<400> 148

Met Ala Leu Leu Phe Ser Leu Ile Leu Ala Ile Cys Thr Arg Pro Gly
 1 5 10 15

Phe Leu Ala Ser Pro Ser Gly Val Arg Leu Val Gly Gly Leu His Arg
 20 25 30

Cys Glu Gly Arg Val Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val
 35 40 45

Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu
 50 55 60

Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu
 65 70 75 80

Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys
 85 90 95

Thr Gly Thr Glu Asp Thr Leu Ala Gln Cys Glu Gln Glu Glu Val Tyr
 100 105 110

Asp Cys Ser His Asp Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu
 115 120 125
 Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro
 130 135 140
 Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr
 145 150 155 160
 Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys
 165 170 175
 Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn
 180 185 190
 Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys
 195 200 205
 Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly
 210 215 220
 Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp
 225 230 235 240
 Pro Phe Asp Leu Arg Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg
 245 250 255
 Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn
 260 265 270
 Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly
 275 280 285
 Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly
 290 295 300
 Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln
 305 310 315 320
 Ser Leu Glu Gln Cys Gln His Arg Phe Trp Gly Phe His Asp Cys Thr
 325 330 335
 His Gln Glu Asp Val Ala Val Ile Cys Ser Val
 340 345

<210> 149

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

<400> 149

ttcagctcat caccttcacc tgcc

24

<210> 150

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 150

ggctcataca aaataccact aggg

24

<210> 151

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 151

gggcctccac cgctgtgaag ggcggtgga ggtggaacag aaaggccagt

50

<210> 152

<211> 1427

<212> DNA

<213> Homo sapiens

<400> 152

actgcactcg gttctatcga ttgaattccc cggggatcct ctagagatcc ctcgacctcg 60
 acccagcgt ccgcggacgc gtgggaggac gcgtgggccc gctaccagga agagtctgcc 120
 gaaggtgaag gccatggact tcatcacctc cacagccatc ctgcccctgc tgttcggtcg 180
 cctgggcgtc ttcggcctct tccggctgct gcagtgggtg cgcgggaagg cctacctgcg 240
 gaatgctgtg gtggtgatca caggcggcac ctcagggtg ggcaaagaat gtgcaaaagt 300
 cttctatgct gcgggtgcta aactggtgct ctgtggccgg aatggtgggg ccctagaaga 360
 gctcatcaga gaacttaccg cttctcatgc caccaagggtg cagacacaca agccttactt 420
 ggtgaccttc gacctcacag actctggggc catagtgtga gcagcagctg agatcctgca 480
 gtgctttggc tatgtcgaca tacttgtcaa caatgctggg atcagctacc gtggtaccat 540
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 catcagcagc atccagggca agatgagcat tccttttcga tcagcatatg cagcctccaa 720
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 ggtgaccgtc atcagccccg gctacatcca caccacaccc tctgtaaatg ccatcaccgc 840
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 ggtggcccag gatgttcttg ctgctgtggg gaagaagaag aaagatgtga tcctggctga 960
 cttactgect tccttggtcg tttatctteg aactctggct cctgggctct tcttcagcct 1020
 catggcctcc agggccagaa aagagcggaa atccaagaac tcctagtact ctgaccagcc 1080

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agggccaggg cagagaagca gcactcttag gcttgcttac tctacaaggg acagttgcat 1140
ttgttgagac tttatggag atttgtctca caagtgggaa agactgaaga aacacatctc 1200
gtgcagatct gctggcagag gacaatcaaa aacgacaaca agcttcttcc cagggtgagg 1260
ggaaacactt aaggaataaa tatggagctg gggtttaaca ctaaaaacta gaaataaaca 1320
tctcaaacag taaaaaaaaa aaaaaagggc ggccgcgact ctagagtcga cctgcagaag 1380
cttgcccgcc atggcccaac ttgtttattg cagcttataa tggttac 1427

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<210> 153

<211> 310

<212> PRT

<213> Homo sapiens

<400> 153

```

Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys
  1              5              10              15

```

```

Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys
          20              25              30

```

```

Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly
          35              40              45

```

```

Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu
          50              55              60

```

```

Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu
          65              70              75              80

```

```

Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu
          85              90              95

```

```

Val Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala
          100             105             110

```

```

Glu Ile Leu Gln Cys Phe Gly Tyr Val Asp Ile Leu Val Asn Asn Ala
          115             120             125

```

```

Gly Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp
          130             135             140

```

```

Lys Arg Val Met Glu Thr Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys
          145             150             155             160

```

```

Ala Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala
          165             170             175

```

```

Ile Ser Ser Ile Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr
          180             185             190

```

```

Ala Ala Ser Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala
          195             200             205

```

```

Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr

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|---|-----|---------|
| 210 | 215 | 220 |
| Ile His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg | | |
| 225 | 230 | 235 240 |
| Tyr Gly Val Met Asp Thr Thr Thr Ala Gln Gly Arg Ser Pro Val Glu | | |
| | 245 | 250 255 |
| Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Lys Asp Val | | |
| | 260 | 265 270 |
| Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu | | |
| | 275 | 280 285 |
| Ala Pro Gly Leu Phe Phe Ser Leu Met Ala Ser Arg Ala Arg Lys Glu | | |
| | 290 | 295 300 |

Arg Lys Ser Lys Asn Ser
305 310

<210> 154

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 154

ggtgctaaac tgggtgctctg tggc

24

<210> 155

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 155

cagggcaaga tgagcattcc

20

<210> 156

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 156
tcatactggtt ccatctcggc acgc

24

<210> 157
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 157
aatggtgggg ccctagaaga gctcatcaga gaactcaccg cttctcatgc

50

<210> 158
<211> 1771
<212> DNA
<213> Homo sapiens

<400> 158
cccacgcgtc cgctggtggt agatcgagca accctctaaa agcagtttag agtggtaaaa 60
aaaaaaaaaa acacacccaaa cgctcgcagc cacaaaaggg atgaaatttc ttctggacat 120
cctcctgctt ctcccgttac tgatcgtctg ctccctagag tccttcgtga agctttttat 180
tcctaagagg agaaaatcag tcaccggcga aatcgtgctg attacaggag ctgggcatgg 240
aattgggaga ctgactgcct atgaatttgc taaacttaaa agcaagctgg ttctctggga 300
tataaataag catggactgg aggaaacagc tgccaaatgc aagggactgg gtgccaaggt 360
tcataccttt gtggtagact gcagcaaccg agaagatatt tacagctctg caaagaaggt 420
gaaggcagaa attggagatg ttagtatttt agtaataat gctgggtgtag tctatacatc 480
agatttggtt gctacacaag atcctcagat tgaaaagact tttgaagtta atgtacttgc 540
acatttctgg actacaaagg catttcttcc tgcaatgacg aagaataacc atggccatat 600
tgtcactgtg gcttcggcag ctggacatgt ctcggtcccc ttcttactgg cttactgttc 660
aagcaagttt gctgctgttg gatctcataa aactttgaca gatgaactgg ctgccttaca 720
aataactgga gtcaaaaaca catgtctgtg tcctaatttc gtaaacactg gttcatcaa 780
aatccaagt acaagtttgg gaccactctt ggaacctgag gaagtggtaa acaggctgat 840
gcatgggatt ctgactgagc agaagatgat ttttattcca tcttctatag cttttttaac 900
aacattggaa aggatccttc ctgagcgttt cctggcagtt ttaaaacgaa aaatcagtg 960
taagtttgat gcagttattg gatataaaat gaaagcgcaa taagcaccta gttttctgaa 1020
aactgattta ccaggtttag gttgatgtca tctaatagtg ccagaatttt aatgtttgaa 1080
cttctgtttt ttctaattat cccattttct tcaatatcat ttttgaggct ttggcagtc 1140
tcatttacta ccacttgttc tttagccaaa agctgattac atatgatata aacagagaaa 1200
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taatttccaa gattatttgt ggctcacctg aaggctttgc aaaatttgta ccataaccgt 1320
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a a 1771

<210> 159

<211> 300

<212> PRT

<213> Homo sapiens

<400> 159

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Met Lys Phe Leu Leu Asp Ile Leu Leu Leu Leu Pro Leu Leu Ile Val
  1             5             10             15

Cys Ser Leu Glu Ser Phe Val Lys Leu Phe Ile Pro Lys Arg Arg Lys
      20             25             30

Ser Val Thr Gly Glu Ile Val Leu Ile Thr Gly Ala Gly His Gly Ile
      35             40             45

Gly Arg Leu Thr Ala Tyr Glu Phe Ala Lys Leu Lys Ser Lys Leu Val
      50             55             60

Leu Trp Asp Ile Asn Lys His Gly Leu Glu Glu Thr Ala Ala Lys Cys
      65             70             75             80

Lys Gly Leu Gly Ala Lys Val His Thr Phe Val Val Asp Cys Ser Asn
      85             90             95

Arg Glu Asp Ile Tyr Ser Ser Ala Lys Lys Val Lys Ala Glu Ile Gly
      100            105            110

Asp Val Ser Ile Leu Val Asn Asn Ala Gly Val Val Tyr Thr Ser Asp
      115            120            125

Leu Phe Ala Thr Gln Asp Pro Gln Ile Glu Lys Thr Phe Glu Val Asn
      130            135            140

Val Leu Ala His Phe Trp Thr Thr Lys Ala Phe Leu Pro Ala Met Thr
      145            150            155            160

Lys Asn Asn His Gly His Ile Val Thr Val Ala Ser Ala Ala Gly His
      165            170            175

Val Ser Val Pro Phe Leu Leu Ala Tyr Cys Ser Ser Lys Phe Ala Ala
      180            185            190

Val Gly Phe His Lys Thr Leu Thr Asp Glu Leu Ala Ala Leu Gln Ile
      195            200            205

Thr Gly Val Lys Thr Thr Cys Leu Cys Pro Asn Phe Val Asn Thr Gly
      210            215            220

Phe Ile Lys Asn Pro Ser Thr Ser Leu Gly Pro Thr Leu Glu Pro Glu
      225            230            235            240

Glu Val Val Asn Arg Leu Met His Gly Ile Leu Thr Glu Gln Lys Met
      245            250            255

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Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu Arg Ile
 260 265 270

Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile Ser Val Lys
 275 280 285

Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln
 290 295 300

<210> 160

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 160

ggtgaaggca gaaattggag atg 23

<210> 161

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 161

atcccatgca tcagcctgtt tacc 24

<210> 162

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 162

gctggtgtag tctatacatc agatttgttt gctacacaag atcctcag 48

<210> 163

<211> 2076

<212> DNA

<213> Homo sapiens

<400> 163

cccacgcgtc cgcggacgcg tgggtcgact agttctagat cgcgagcggc cgcccgcggc 60
 tcagggagga gcaccgactg cgccgcaccc tgagagatgg ttggtgccat gtggaagggtg 120

attgtttcgc tggctcctggt gatgcctggc ccctgtgatg ggctgtttcg ctccctatac 180
 agaagtgttt ccatgccacc taaggagagc tcaggacagc cattatctct cacccttac 240
 attgaagctg ggaagatcca aaaaggaaga gaattgagtt tggtcggccc tttcccagga 300
 ctgaacatga agagttatgc cggcttcctc accgtgaata agacttacaa cagcaacctc 360
 ttcttctggt tcttcccagc tcagatacag ccagaagatg cccagtagt tctctggcta 420
 caggggtgggc cgggaggttc atccatgttt ggactctttg tggaaacatgg gccttatgtt 480
 gtcacaagta acatgacctt gcgtgacaga gacttccctt ggaccacaac gctctccatg 540
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 gcagtcaatg aggacgatgt agcacgggat ttatacagt cactaattca gtttttccag 660
 atatttcctg aatataaaaa taatgacttt tatgtcactg gggagtctta tgcagggaaa 720
 tatgtgccag ccattgcaca cctcatccat tccctcaacc ctgtgagaga ggtgaagatc 780
 aacctgaacg gaattgctat tggagatgga tattctgatc ccgaatcaat tatagggggc 840
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 gtgtttggaa atattattgg ataagaatag ctcaattatc ccaaataaat ggatgaagct 1980
 ataatagttt tggggaaaag attctcaaat gtataaagtc ttagaacaaa agaattcttt 2040
 gaaataaaaa tattatatat aaaagtaaaa aaaaaa 2076

<210> 164

<211> 476

<212> PRT

<213> Homo sapiens

<400> 164

Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met
 1 5 10 15

Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser Val Ser
 20 25 30

Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr
 35 40 45

Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly
 50 55 60

Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val

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|---|---------------------------------|-----------------------------|--|----|-----|-----|
| 65 | | 70 | | 75 | | 80 |
| Asn Lys Thr Tyr | Asn Ser Asn Leu Phe | Phe Trp Phe Phe Pro Ala Gln | | | | |
| | 85 | 90 | | | 95 | |
| Ile Gln Pro Glu Asp Ala Pro Val | Val Leu Trp Leu Gln Gly Gly Pro | | | | | |
| | 100 | 105 | | | 110 | |
| Gly Gly Ser Ser Met Phe Gly Leu Phe Val Glu His Gly Pro Tyr Val | | | | | | |
| | 115 | 120 | | | 125 | |
| Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp Thr Thr | | | | | | |
| | 130 | 135 | | | 140 | |
| Thr Leu Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly Phe Ser | | | | | | |
| | 145 | 150 | | | 155 | 160 |
| Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp Val Ala | | | | | | |
| | 165 | 170 | | | 175 | |
| Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe Pro Glu | | | | | | |
| | 180 | 185 | | | 190 | |
| Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala Gly Lys | | | | | | |
| | 195 | 200 | | | 205 | |
| Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro Val Arg | | | | | | |
| | 210 | 215 | | | 220 | |
| Glu Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp Gly Tyr Ser | | | | | | |
| | 225 | 230 | | | 235 | 240 |
| Asp Pro Glu Ser Ile Ile Gly Gly Tyr Ala Glu Phe Leu Tyr Gln Ile | | | | | | |
| | 245 | 250 | | | 255 | |
| Gly Leu Leu Asp Glu Lys Gln Lys Lys Tyr Phe Gln Lys Gln Cys His | | | | | | |
| | 260 | 265 | | | 270 | |
| Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu Ala Phe Glu | | | | | | |
| | 275 | 280 | | | 285 | |
| Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp Pro Ser Tyr | | | | | | |
| | 290 | 295 | | | 300 | |
| Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe Leu Arg Cys | | | | | | |
| | 305 | 310 | | | 315 | 320 |
| Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser Leu Pro | | | | | | |
| | 325 | 330 | | | 335 | |
| Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn Asp Gly | | | | | | |
| | 340 | 345 | | | 350 | |

Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys
 355 360 365

Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn
 370 375 380

Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu
 385 390 395 400

Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys
 405 410 415

Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile
 420 425 430

Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly Gly His
 435 440 445

Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg
 450 455 460

Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly
 465 470 475

<210> 165

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 165

ttccatgcca cctaagggag actc

24

<210> 166

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 166

tggatgaggt gtgcaatggc tggc

24

<210> 167

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 167

agctctcaga ggctggtcat aggg

24

<210> 168

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 168

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50

<210> 169

<211> 2477

<212> DNA

<213> Homo sapiens

<400> 169

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```

<210> 170

<211> 552

<212> PRT

<213> Homo sapiens

<400> 170

```

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      20             25             30

Gln Pro Gly Lys Val Glu Gln Met Ser Thr His Arg Ser Arg Leu Leu
      35             40             45

Thr Ala Ala Pro Leu Ser Met Glu Gln Arg Gln Pro Trp Pro Arg Ala
      50             55             60

Leu Glu Val Asp Ser Arg Ser Val Val Leu Leu Ser Val Val Trp Val
      65             70             75             80

Leu Leu Ala Pro Pro Ala Ala Gly Met Pro Gln Phe Ser Thr Phe His
      85             90             95

Ser Glu Asn Arg Asp Trp Thr Phe Asn His Leu Thr Val His Gln Gly
      100            105            110

Thr Gly Ala Val Tyr Val Gly Ala Ile Asn Arg Val Tyr Lys Leu Thr
      115            120            125

Gly Asn Leu Thr Ile Gln Val Ala His Lys Thr Gly Pro Glu Glu Asp
      130            135            140

Asn Lys Ser Arg Tyr Pro Pro Leu Ile Val Gln Pro Cys Ser Glu Val
      145            150            155            160

Leu Thr Leu Thr Asn Asn Val Asn Lys Leu Leu Ile Ile Asp Tyr Ser
      165            170            175

```

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Asn | Arg | Leu | Ala | Cys | Gly | Ser | Leu | Tyr | Gln | Gly | Val | Cys | Lys | |
| | | | 180 | | | | 185 | | | | | | 190 | | |
| Leu | Leu | Arg | Leu | Asp | Asp | Leu | Phe | Ile | Leu | Val | Glu | Pro | Ser | His | Lys |
| | | | 195 | | | | 200 | | | | | | 205 | | |
| Lys | Glu | His | Tyr | Leu | Ser | Ser | Val | Asn | Lys | Thr | Gly | Thr | Met | Tyr | Gly |
| | | | 210 | | | | 215 | | | | | | 220 | | |
| Val | Ile | Val | Arg | Ser | Glu | Gly | Glu | Asp | Gly | Lys | Leu | Phe | Ile | Gly | Thr |
| | | | 225 | | | | 230 | | | | | | 235 | 240 | |
| Ala | Val | Asp | Gly | Lys | Gln | Asp | Tyr | Phe | Pro | Thr | Leu | Ser | Ser | Arg | Lys |
| | | | 245 | | | | 250 | | | | | | 255 | | |
| Leu | Pro | Arg | Asp | Pro | Glu | Ser | Ser | Ala | Met | Leu | Asp | Tyr | Glu | Leu | His |
| | | | 260 | | | | 265 | | | | | | 270 | | |
| Ser | Asp | Phe | Val | Ser | Ser | Leu | Ile | Lys | Ile | Pro | Ser | Asp | Thr | Leu | Ala |
| | | | 275 | | | | 280 | | | | | | 285 | | |
| Leu | Val | Ser | His | Phe | Asp | Ile | Phe | Tyr | Ile | Tyr | Gly | Phe | Ala | Ser | Gly |
| | | | 290 | | | | 295 | | | | | | 300 | | |
| Gly | Phe | Val | Tyr | Phe | Leu | Thr | Val | Gln | Pro | Glu | Thr | Pro | Glu | Gly | Val |
| | | | 305 | | | | 310 | | | | | | 315 | 320 | |
| Ala | Ile | Asn | Ser | Ala | Gly | Asp | Leu | Phe | Tyr | Thr | Ser | Arg | Ile | Val | Arg |
| | | | 325 | | | | 330 | | | | | | 335 | | |
| Leu | Cys | Lys | Asp | Asp | Pro | Lys | Phe | His | Ser | Tyr | Val | Ser | Leu | Pro | Phe |
| | | | 340 | | | | 345 | | | | | | 350 | | |
| Gly | Cys | Thr | Arg | Ala | Gly | Val | Glu | Tyr | Arg | Leu | Leu | Gln | Ala | Ala | Tyr |
| | | | 355 | | | | 360 | | | | | | 365 | | |
| Leu | Ala | Lys | Pro | Gly | Asp | Ser | Leu | Ala | Gln | Ala | Phe | Asn | Ile | Thr | Ser |
| | | | 370 | | | | 375 | | | | | | 380 | | |
| Gln | Asp | Asp | Val | Leu | Phe | Ala | Ile | Phe | Ser | Lys | Gly | Gln | Lys | Gln | Tyr |
| | | | 385 | | | | 390 | | | | | | 395 | 400 | |
| His | His | Pro | Pro | Asp | Asp | Ser | Ala | Leu | Cys | Ala | Phe | Pro | Ile | Arg | Ala |
| | | | 405 | | | | 410 | | | | | | 415 | | |
| Ile | Asn | Leu | Gln | Ile | Lys | Glu | Arg | Leu | Gln | Ser | Cys | Tyr | Gln | Gly | Glu |
| | | | 420 | | | | 425 | | | | | | 430 | | |
| Gly | Asn | Leu | Glu | Leu | Asn | Trp | Leu | Leu | Gly | Lys | Asp | Val | Gln | Cys | Thr |
| | | | 435 | | | | 440 | | | | | | 445 | | |
| Lys | Ala | Pro | Val | Pro | Ile | Asp | Asp | Asn | Phe | Cys | Gly | Leu | Asp | Ile | Asn |

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<210> 171
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
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<210> 172
<211> 24
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 172
ctttctgccct ttggagaaga tggc 24

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<210> 173
<211> 43
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 173
ggactcactg gcccaggcct tcaatatcac cagccaggac gat 42

<210> 174
<211> 3106
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (1683)
<223> a, t, c or g

<400> 174
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tgctggctcgt cttgggcttc ctggtgctcc gcaggctgga ctggagcacc ctggctccctc 180
tgcggtcccg ccacgcacag ctggggctgc aggccaaggg ctggaacttc atgctggagg 240
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cagaaaaagt gctgaaacgt gcccttgac cggacgtcac agccctgcga gcatctgctg 2340
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<210> 175

<211> 636

<212> PRT

<213> Homo sapiens

<220>

<221> MOD_RES

<222> (539)

<223> Any amino acid

<400> 175

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Met Thr Thr Trp Ser Leu Arg Arg Arg Pro Ala Arg Thr Leu Gly Leu
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```

```

Leu Leu Leu Val Val Leu Gly Phe Leu Val Leu Arg Arg Leu Asp Trp
      20              25              30

```

```

Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly Leu Gln
    35              40              45

```

```

Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp Ile Phe
    50              55              60

```

```

Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp Arg Asp
    65              70              75              80

```

```

Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr Thr Tyr
      85              90              95

```

```

Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp Phe Ser
    100              105              110

```

```

Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu Ile Gly
    115              120              125

```

```

Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu Met Asp
    130              135              140

```

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Gly | Gly | Leu | Pro | Ser | Trp | Leu | Leu | Gln | Asp | Pro | Gly | Met | Arg | Leu |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Arg | Thr | Thr | Tyr | Lys | Gly | Phe | Thr | Glu | Ala | Val | Asp | Leu | Tyr | Phe | Asp |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| His | Leu | Met | Ser | Arg | Val | Val | Pro | Leu | Gln | Tyr | Lys | Arg | Gly | Gly | Pro |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Ile | Ile | Ala | Val | Gln | Val | Glu | Asn | Glu | Tyr | Gly | Ser | Tyr | Asn | Lys | Asp |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Pro | Ala | Tyr | Met | Pro | Tyr | Val | Lys | Lys | Ala | Leu | Glu | Asp | Arg | Gly | Ile |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Val | Glu | Leu | Leu | Leu | Thr | Ser | Asp | Asn | Lys | Asp | Gly | Leu | Ser | Lys | Gly |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Ile | Val | Gln | Gly | Val | Leu | Ala | Thr | Ile | Asn | Leu | Gln | Ser | Thr | His | Glu |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Leu | Gln | Leu | Leu | Thr | Thr | Phe | Leu | Phe | Asn | Val | Gln | Gly | Thr | Gln | Pro |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Lys | Met | Val | Met | Glu | Tyr | Trp | Thr | Gly | Trp | Phe | Asp | Ser | Trp | Gly | Gly |
| | | 275 | | | | | 280 | | | | | 285 | | | |
| Pro | His | Asn | Ile | Leu | Asp | Ser | Ser | Glu | Val | Leu | Lys | Thr | Val | Ser | Ala |
| | | 290 | | | | 295 | | | | | 300 | | | | |
| Ile | Val | Asp | Ala | Gly | Ser | Ser | Ile | Asn | Leu | Tyr | Met | Phe | His | Gly | Gly |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| Thr | Asn | Phe | Gly | Phe | Met | Asn | Gly | Ala | Met | His | Phe | His | Asp | Tyr | Lys |
| | | | | 325 | | | | | 330 | | | | | 335 | |
| Ser | Asp | Val | Thr | Ser | Tyr | Asp | Tyr | Asp | Ala | Val | Leu | Thr | Glu | Ala | Gly |
| | | | 340 | | | | | 345 | | | | | 350 | | |
| Asp | Tyr | Thr | Ala | Lys | Tyr | Met | Lys | Leu | Arg | Asp | Phe | Phe | Gly | Ser | Ile |
| | | 355 | | | | | 360 | | | | | 365 | | | |
| Ser | Gly | Ile | Pro | Leu | Pro | Pro | Pro | Pro | Asp | Leu | Leu | Pro | Lys | Met | Pro |
| | 370 | | | | | 375 | | | | | 380 | | | | |
| Tyr | Glu | Pro | Leu | Thr | Pro | Val | Leu | Tyr | Leu | Ser | Leu | Trp | Asp | Ala | Leu |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 |
| Lys | Tyr | Leu | Gly | Glu | Pro | Ile | Lys | Ser | Glu | Lys | Pro | Ile | Asn | Met | Glu |
| | | | | 405 | | | | | 410 | | | | | 415 | |
| Asn | Leu | Pro | Val | Asn | Gly | Gly | Asn | Gly | Gln | Ser | Phe | Gly | Tyr | Ile | Leu |
| | | | 420 | | | | | 425 | | | | | 430 | | |

Tyr Glu Thr Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His Val His
435 440 445

Asp Arg Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe Leu Asp
450 455 460

Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr Thr Val
465 470 475 480

Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly Glu Asn
485 490 495

Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu Asn Asp
500 505 510

Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys Lys Ser
515 520 525

Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Xaa Ser Leu Pro Glu Thr
530 535 540

Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser Ser Thr
545 550 555 560

Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly Val Val
565 570 575

Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly Pro Gln
580 585 590

Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln
595 600 605

Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln Phe Thr
610 615 620

Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys
625 630 635

<210> 176

<211> 2505

<212> DNA

<213> Homo sapiens

<400> 176

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aaggggagca aagccggggt cggcccaggc ccccaggac ctccatctcc caatggttga 180
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tatttttgac ggggaaactg ggggtccaaac tggatatctt ggtggagaac atggggaggc 1680
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agcctatcct caatagcact agtactttgc acaggacaca tatcaattcc ctttcagctg 2160
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ggtggctcat gcctgtaatc ccagcacttt gggaggtgga gacgggtgga ttacctgagg 2280
tcaggacttc aagaccagcc tggccaacat ggtgaaaccc cgtctccact aaaaatacaa 2340
aaattagccg ggcgtgatgg tgggcacctc taatcccagc tacttgggag gctgagggca 2400
ggagaattgc ttgaatccag gaggcagagg ttgcagtgag tggagggtgt accactgcac 2460
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```

<210> 177

<211> 654

<212> PRT

<213> Homo sapiens

<400> 177

```

Met Ala Pro Lys Lys Leu Ser Cys Leu Arg Ser Leu Leu Leu Pro Leu
  1              5              10              15

```

```

Ser Leu Thr Leu Leu Leu Pro Gln Ala Asp Thr Arg Ser Phe Val Val
      20              25              30

```

```

Asp Arg Gly His Asp Arg Phe Leu Leu Asp Gly Ala Pro Phe Arg Tyr
  35              40              45

```

```

Val Ser Gly Ser Leu His Tyr Phe Arg Val Pro Arg Val Leu Trp Ala
  50              55              60

```

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Arg | Leu | Leu | Lys | Met | Arg | Trp | Ser | Gly | Leu | Asn | Ala | Ile | Gln | Phe | 65 | 70 | 75 | 80 |
| Tyr | Val | Pro | Trp | Asn | Tyr | His | Glu | Pro | Gln | Pro | Gly | Val | Tyr | Asn | Phe | 85 | 90 | 95 | |
| Asn | Gly | Ser | Arg | Asp | Leu | Ile | Ala | Phe | Leu | Asn | Glu | Ala | Ala | Leu | Ala | 100 | 105 | 110 | |
| Asn | Leu | Leu | Val | Ile | Leu | Arg | Pro | Gly | Pro | Tyr | Ile | Cys | Ala | Glu | Trp | 115 | 120 | 125 | |
| Glu | Met | Gly | Gly | Leu | Pro | Ser | Trp | Leu | Leu | Arg | Lys | Pro | Glu | Ile | His | 130 | 135 | 140 | |
| Leu | Arg | Thr | Ser | Asp | Pro | Asp | Phe | Leu | Ala | Ala | Val | Asp | Ser | Trp | Phe | 145 | 150 | 155 | 160 |
| Lys | Val | Leu | Leu | Pro | Lys | Ile | Tyr | Pro | Trp | Leu | Tyr | His | Asn | Gly | Gly | 165 | 170 | 175 | |
| Asn | Ile | Ile | Ser | Ile | Gln | Val | Glu | Asn | Glu | Tyr | Gly | Ser | Tyr | Arg | Ala | 180 | 185 | 190 | |
| Cys | Asp | Phe | Ser | Tyr | Met | Arg | His | Leu | Ala | Gly | Leu | Phe | Arg | Ala | Leu | 195 | 200 | 205 | |
| Leu | Gly | Glu | Lys | Ile | Leu | Leu | Phe | Thr | Thr | Asp | Gly | Pro | Glu | Gly | Leu | 210 | 215 | 220 | |
| Lys | Cys | Gly | Ser | Leu | Arg | Gly | Leu | Tyr | Thr | Thr | Val | Asp | Phe | Gly | Pro | 225 | 230 | 235 | 240 |
| Ala | Asp | Asn | Met | Thr | Lys | Ile | Phe | Thr | Leu | Leu | Arg | Lys | Tyr | Glu | Pro | 245 | 250 | 255 | |
| His | Gly | Pro | Leu | Val | Asn | Ser | Glu | Tyr | Tyr | Thr | Gly | Trp | Leu | Asp | Tyr | 260 | 265 | 270 | |
| Trp | Gly | Gln | Asn | His | Ser | Thr | Arg | Ser | Val | Ser | Ala | Val | Thr | Lys | Gly | 275 | 280 | 285 | |
| Leu | Glu | Asn | Met | Leu | Lys | Leu | Gly | Ala | Ser | Val | Asn | Met | Tyr | Met | Phe | 290 | 295 | 300 | |
| His | Gly | Gly | Thr | Asn | Phe | Gly | Tyr | Trp | Asn | Gly | Ala | Asp | Lys | Lys | Gly | 305 | 310 | 315 | 320 |
| Arg | Phe | Leu | Pro | Ile | Thr | Thr | Ser | Tyr | Asp | Tyr | Asp | Ala | Pro | Ile | Ser | 325 | 330 | 335 | |
| Glu | Ala | Gly | Asp | Pro | Thr | Pro | Lys | Leu | Phe | Ala | Leu | Arg | Asp | Val | Ile | | | | |

| | | |
|---|-----|-----|
| 340 | 345 | 350 |
| Ser Lys Phe Gln Glu Val Pro Leu Gly Pro Leu Pro Pro Pro Ser Pro | | |
| 355 | 360 | 365 |
| Lys Met Met Leu Gly Pro Val Thr Leu His Leu Val Gly His Leu Leu | | |
| 370 | 375 | 380 |
| Ala Phe Leu Asp Leu Leu Cys Pro Arg Gly Pro Ile His Ser Ile Leu | | |
| 385 | 390 | 400 |
| Pro Met Thr Phe Glu Ala Val Lys Gln Asp His Gly Phe Met Leu Tyr | | |
| | 405 | 410 |
| Arg Thr Tyr Met Thr His Thr Ile Phe Glu Pro Thr Pro Phe Trp Val | | |
| | 420 | 425 |
| Pro Asn Asn Gly Val His Asp Arg Ala Tyr Val Met Val Asp Gly Val | | |
| | 435 | 440 |
| Phe Gln Gly Val Val Glu Arg Asn Met Arg Asp Lys Leu Phe Leu Thr | | |
| | 450 | 455 |
| Gly Lys Leu Gly Ser Lys Leu Asp Ile Leu Val Glu Asn Met Gly Arg | | |
| 465 | 470 | 475 |
| Leu Ser Phe Gly Ser Asn Ser Ser Asp Phe Lys Gly Leu Leu Lys Pro | | |
| | 485 | 490 |
| Pro Ile Leu Gly Gln Thr Ile Leu Thr Gln Trp Met Met Phe Pro Leu | | |
| | 500 | 505 |
| Lys Ile Asp Asn Leu Val Lys Trp Trp Phe Pro Leu Gln Leu Pro Lys | | |
| | 515 | 520 |
| Trp Pro Tyr Pro Gln Ala Pro Ser Gly Pro Thr Phe Tyr Ser Lys Thr | | |
| | 530 | 535 |
| Phe Pro Ile Leu Gly Ser Val Gly Asp Thr Phe Leu Tyr Leu Pro Gly | | |
| 545 | 550 | 555 |
| Trp Thr Lys Gly Gln Val Trp Ile Asn Gly Phe Asn Leu Gly Arg Tyr | | |
| | 565 | 570 |
| Trp Thr Lys Gln Gly Pro Gln Gln Thr Leu Tyr Val Pro Arg Phe Leu | | |
| | 580 | 585 |
| Leu Phe Pro Arg Gly Ala Leu Asn Lys Ile Thr Leu Leu Glu Leu Glu | | |
| | 595 | 600 |
| Asp Val Pro Leu Gln Pro Gln Val Gln Phe Leu Asp Lys Pro Ile Leu | | |
| | 610 | 615 |
| | | 620 |

Asn Ser Thr Ser Thr Leu His Arg Thr His Ile Asn Ser Leu Ser Ala
 625 630 635 640

Asp Thr Leu Ser Ala Ser Glu Pro Met Glu Leu Ser Gly His
 645 650

<210> 178

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 178

tggctactcc aagaccctgg catg

24

<210> 179

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 179

tggacaaaatc cccttgctca gccc

24

<210> 180

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 180

gggcttcacc gaagcagtgg acctttattt tgaccacctg atgtccaggg

50

<210> 181

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 181

ccagctatga ctatgatgca cc

22

<210> 182
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 182
 tggcaccacag aatggtgttg gctc 24

<210> 183
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 183
 cgagatgtca tcagcaagtt ccaggaagtt cctttgggac ctttacctcc 50

<210> 184
 <211> 1947
 <212> DNA
 <213> Homo sapiens

<400> 184
 gctttgaaca cgtctgcaag cccaaagttg agcatctgat tggttatgag gtatttgagt 60
 gcaccacaaa tatggcttac atggtgaaaa agcttctcat cagttacata tccattattt 120
 gtgtttatgg ctttatctgc ctctacactc tcttctgggt attcaggata cctttgaagg 180
 aatattcttt cgaaaaagtc agagaagaga gcagttttag tgacattcca gatgtcaaaa 240
 acgattttgc gttccttctt cacatggtag accagtatga ccagctatat tccaagcgtt 300
 ttgggtgtgtt cttgtcagaa gttagtgaat ataaacttag ggaaattagt ttgaaccatg 360
 agtggacatt tgaaaaactc aggcagcaca tttcacgcaa cgcccaggac aagcaggagt 420
 tgcactctgtt catgctgtcg ggggtgcccg atgctgtctt tgacctcaca gacctggatg 480
 tgctaaagct tgaactaatt ccagaagcta aaattcctgc taagatttct caaatgacta 540
 acctccaaga gctccacctc tgccactgcc ctgcaaaaagt tgaacagact gcttttagct 600
 ttcttcgcga tcacttgaga tgcccttcacg tgaagttcac tgatgtggct gaaattcctg 660
 cctgggtgta tttgctcaaa aaccttcgag agttgtactt aataggcaat ttgaactctg 720
 aaaacaataa gatgatagga cttgaatctc tccgagagtt ggggcacctt aagattctcc 780
 acgtgaagag caatttgacc aaagttccct ccaacattac agatgtggct ccacatctta 840
 caaagttagt cattcataat gacggcacta aactcttggt actgaacagc ctttaagaaaa 900
 tgatgaatgt cgctgagctg gaactccaga actgtgagct agagagaatc ccacatgcta 960
 ttttcagcct ctctaattta caggaactgg atttaaagtc caataacatt cgcacaattg 1020
 aggaaatcat cagtttccag catTTaaaac gactgacttg tttaaaatta tggcataaca 1080
 aaattgttac tattcctccc tctattaccc atgtcaaaaa cttggagtca ctttatttct 1140
 ctaacaacaa gctcgaatcc ttaccagtgg cagtatttag ttacagaaa ctccagatgct 1200
 tagatgtgag ctacaacaac atttcaatga ttccaataga aataggattg cttcagaacc 1260
 tgcagcattt gcatatcact gggaacaaaag tggacattct gccaaaacaa ttgttttaaa 1320

```

gcataaagtt gaggactttg aatctgggac agaactgcat cacctcactc ccagagaaaag 1380
ttggtcagct ctcccagctc actcagctgg agctgaaggg gaactgcttg gaccgcctgc 1440
cagcccagct gggccagtgt cggatgctca agaaaagcgg gcttggttg gaagatcacc 1500
tttttgatac cctgccactc gaagtcaaag aggcatgaa tcaagacata aatattccct 1560
ttgcaaagtg gattttaaact aagataatat atgcacagtg atgtgcagga acaacttcc 1620
agattgcaag tgctcacgta caagttatta caagataatg catttttagga gtagatacat 1680
ctttttaaagt aaaacagaga ggatgcatag aaggctgata gaagacataa ctgaatgttc 1740
aatgtttgta gggttttaag tcattcattt ccaaatacatt tttttttttc ttttggggaa 1800
aggggaaggaa aaattataat cactaatctt ggttcttttt aaattgtttg taacttggat 1860
gctgccgcta ctgaatgttt acaaattgct tgcttcttaa agtaaataat taaattgaca 1920
ttttcttact aaaaaaaaaa aaaaaaa 1947

```

<210> 185

<211> 501

<212> PRT

<213> Homo sapiens

<400> 185

```

Met Ala Tyr Met Leu Lys Lys Leu Leu Ile Ser Tyr Ile Ser Ile Ile
  1             5             10             15

```

```

Cys Val Tyr Gly Phe Ile Cys Leu Tyr Thr Leu Phe Trp Leu Phe Arg
          20             25             30

```

```

Ile Pro Leu Lys Glu Tyr Ser Phe Glu Lys Val Arg Glu Glu Ser Ser
      35             40             45

```

```

Phe Ser Asp Ile Pro Asp Val Lys Asn Asp Phe Ala Phe Leu Leu His
      50             55             60

```

```

Met Val Asp Gln Tyr Asp Gln Leu Tyr Ser Lys Arg Phe Gly Val Phe
      65             70             75             80

```

```

Leu Ser Glu Val Ser Glu Asn Lys Leu Arg Glu Ile Ser Leu Asn His
          85             90             95

```

```

Glu Trp Thr Phe Glu Lys Leu Arg Gln His Ile Ser Arg Asn Ala Gln
      100             105             110

```

```

Asp Lys Gln Glu Leu His Leu Phe Met Leu Ser Gly Val Pro Asp Ala
      115             120             125

```

```

Val Phe Asp Leu Thr Asp Leu Asp Val Leu Lys Leu Glu Leu Ile Pro
      130             135             140

```

```

Glu Ala Lys Ile Pro Ala Lys Ile Ser Gln Met Thr Asn Leu Gln Glu
      145             150             155             160

```

```

Leu His Leu Cys His Cys Pro Ala Lys Val Glu Gln Thr Ala Phe Ser
          165             170             175

```

```

Phe Leu Arg Asp His Leu Arg Cys Leu His Val Lys Phe Thr Asp Val
          180             185             190

```

Ala Glu Ile Pro Ala Trp Val Tyr Leu Leu Lys Asn Leu Arg Glu Leu
 195 200 205
 Tyr Leu Ile Gly Asn Leu Asn Ser Glu Asn Asn Lys Met Ile Gly Leu
 210 215 220
 Glu Ser Leu Arg Glu Leu Arg His Leu Lys Ile Leu His Val Lys Ser
 225 230 235 240
 Asn Leu Thr Lys Val Pro Ser Asn Ile Thr Asp Val Ala Pro His Leu
 245 250 255
 Thr Lys Leu Val Ile His Asn Asp Gly Thr Lys Leu Leu Val Leu Asn
 260 265 270
 Ser Leu Lys Lys Met Met Asn Val Ala Glu Leu Glu Leu Gln Asn Cys
 275 280 285
 Glu Leu Glu Arg Ile Pro His Ala Ile Phe Ser Leu Ser Asn Leu Gln
 290 295 300
 Glu Leu Asp Leu Lys Ser Asn Asn Ile Arg Thr Ile Glu Glu Ile Ile
 305 310 315 320
 Ser Phe Gln His Leu Lys Arg Leu Thr Cys Leu Lys Leu Trp His Asn
 325 330 335
 Lys Ile Val Thr Ile Pro Pro Ser Ile Thr His Val Lys Asn Leu Glu
 340 345 350
 Ser Leu Tyr Phe Ser Asn Asn Lys Leu Glu Ser Leu Pro Val Ala Val
 355 360 365
 Phe Ser Leu Gln Lys Leu Arg Cys Leu Asp Val Ser Tyr Asn Asn Ile
 370 375 380
 Ser Met Ile Pro Ile Glu Ile Gly Leu Leu Gln Asn Leu Gln His Leu
 385 390 395 400
 His Ile Thr Gly Asn Lys Val Asp Ile Leu Pro Lys Gln Leu Phe Lys
 405 410 415
 Cys Ile Lys Leu Arg Thr Leu Asn Leu Gly Gln Asn Cys Ile Thr Ser
 420 425 430
 Leu Pro Glu Lys Val Gly Gln Leu Ser Gln Leu Thr Gln Leu Glu Leu
 435 440 445
 Lys Gly Asn Cys Leu Asp Arg Leu Pro Ala Gln Leu Gly Gln Cys Arg
 450 455 460
 Met Leu Lys Lys Ser Gly Leu Val Val Glu Asp His Leu Phe Asp Thr

465 470 475 480

Leu Pro Leu Glu Val Lys Glu Ala Leu Asn Gln Asp Ile Asn Ile Pro

 485 490 495

Phe Ala Asn Gly Ile

 500

<210> 186
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 186
 cctccctcta ttacccatgt c 21

<210> 187
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 187
 gaccaacttt ctctgggagt gagg 24

<210> 188
 <211> 47
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 188
 gtcactttat ttctctaaca acaagctcga atccttacca gtggcag 47

<210> 189
 <211> 2917
 <212> DNA
 <213> Homo sapiens

<400> 189
 cccacgcgtc cggccttctc tctggacttt gcatttccat tccttttcat tgacaaaactg 60
 acttttttta tttctttttt tccatctctg ggccagcttg ggatcctagg ccgccctggg 120
 aagacatttg tgttttacac acataaggat ctgtgtttgg ggtttcttct tcctcccctg 180

acattggcat tgcttagtgg ttgtgtgggg agggagacca cgtgggctca gtgcttgctt 240
 gcacttatct gcctaggtac atcgaagtct tttgacctcc atacagtgat tatgcctgtc 300
 atcgctgggtg gtatcctggc ggccttgctc ctgctgatag ttgtcgtgct ctgtctttac 360
 ttcaaaatac acaacgcgct aaaagctgca aaggaacctg aagctgtggc tgtaaaaaat 420
 cacaacccag acaaggtgtg gtgggccaag aacagccagg ccaaaaccat tgccacggag 480
 tcttgtcctg ccctgcagtg ctgtgaagga tatagaatgt gtgccagttt tgattccctg 540
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 agaagaaagg cacagctccc catcagtttc atggaaaata actcagtgcc tgctgggaac 720
 cagctgctgg agatccctac agagagcttc cactgggggc aacccttcca ggaaggagtt 780
 ggggagagag aaccctcact gtggggaatg ctgataaacc agtcacacag ctgctctatt 840
 ctcacacaaa tctaccctt gcgtggctgg aactgacgtt tccctggagg tgtccagaaa 900
 gctgatgtaa cacagagcct ataaaagctg tcggctcctta aggctgcccga gcgccttgcc 960
 aaaatggagc ttgtaagaag gctcatgcca ttgacctct taattctctc ctgtttggcg 1020
 gagctgacaa tggcggaggc tgaaggcaat gcaagctgca cagtcagtct aggggggtgcc 1080
 aatatggcag agaccacaaa agccatgatc ctgcaactca atcccagtga gaactgcacc 1140
 tggacaatag aaagaccaga aaacaaaagc atcagaatta tcttttctta tgtccagctt 1200
 gatccagatg gaagctgtga aagtgaaaac attaaagtct ttgacggaac ctccagcaat 1260
 gggcctctgc tagggcaagt ctgcagtaaa aacgactatg ttctgtatt tgaatcatca 1320
 tccagtacat tgacgtttca aatagttact gactcagcaa gaattcaaag aactgtcttt 1380
 gtcttctact acttcttctc tcttaacatc tctattccaa actgtggcgg ttacctggat 1440
 accttggaag gatccttcac cagccccaat tacccaaagc cgcactctga gctggcttat 1500
 tgtgtgtggc acatacaagt ggagaaaagat tacaagataa aactaaactt caaagagatt 1560
 ttctagaaa tagacaaaca gtgcaaattt gattttcttg ccatctatga tggccctcc 1620
 accaactctg gcctgattgg acaagtctgt ggccgtgtga ctcccacctt cgaatcgtca 1680
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 gtccctctta atggatgtgg tacaatcaga aaggtagaag atcagtcaat tacttacacc 1980
 aatataatca cttttctgc atcctcaact tctgaagtga tcaccctgca gaaacaactc 2040
 cagattattg tgaagtgtga aatgggacat aattctacag tggagataat atacataaca 2100
 gaagatgatg taatacaaaag tcaaaatgca ctgggcaaat ataacaccag catggctctt 2160
 tttgaatcca attctttga aaagactata cttgaatcac catattatgt ggatttgaac 2220
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 ggcctgaaag tgacacacag gcctgcatgt aaaaaaa 2917

<210> 190

<211> 607

<212> PRT

<213> Homo sapiens

<400> 190

Met Glu Leu Val Arg Arg Leu Met Pro Leu Thr Leu Leu Ile Leu Ser
 1 5 10 15
 Cys Leu Ala Glu Leu Thr Met Ala Glu Ala Glu Gly Asn Ala Ser Cys
 20 25 30
 Thr Val Ser Leu Gly Gly Ala Asn Met Ala Glu Thr His Lys Ala Met
 35 40 45
 Ile Leu Gln Leu Asn Pro Ser Glu Asn Cys Thr Trp Thr Ile Glu Arg
 50 55 60
 Pro Glu Asn Lys Ser Ile Arg Ile Ile Phe Ser Tyr Val Gln Leu Asp
 65 70 75 80
 Pro Asp Gly Ser Cys Glu Ser Glu Asn Ile Lys Val Phe Asp Gly Thr
 85 90 95
 Ser Ser Asn Gly Pro Leu Leu Gly Gln Val Cys Ser Lys Asn Asp Tyr
 100 105 110
 Val Pro Val Phe Glu Ser Ser Ser Ser Thr Leu Thr Phe Gln Ile Val
 115 120 125
 Thr Asp Ser Ala Arg Ile Gln Arg Thr Val Phe Val Phe Tyr Tyr Phe
 130 135 140
 Phe Ser Pro Asn Ile Ser Ile Pro Asn Cys Gly Gly Tyr Leu Asp Thr
 145 150 155 160
 Leu Glu Gly Ser Phe Thr Ser Pro Asn Tyr Pro Lys Pro His Pro Glu
 165 170 175
 Leu Ala Tyr Cys Val Trp His Ile Gln Val Glu Lys Asp Tyr Lys Ile
 180 185 190
 Lys Leu Asn Phe Lys Glu Ile Phe Leu Glu Ile Asp Lys Gln Cys Lys
 195 200 205
 Phe Asp Phe Leu Ala Ile Tyr Asp Gly Pro Ser Thr Asn Ser Gly Leu
 210 215 220
 Ile Gly Gln Val Cys Gly Arg Val Thr Pro Thr Phe Glu Ser Ser Ser
 225 230 235 240
 Asn Ser Leu Thr Val Val Leu Ser Thr Asp Tyr Ala Asn Ser Tyr Arg
 245 250 255
 Gly Phe Ser Ala Ser Tyr Thr Ser Ile Tyr Ala Glu Asn Ile Asn Thr
 260 265 270
 Thr Ser Leu Thr Cys Ser Ser Asp Arg Met Arg Val Ile Ile Ser Lys
 275 280 285

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Tyr | Leu | Glu | Ala | Phe | Asn | Ser | Asn | Gly | Asn | Asn | Leu | Gln | Leu | Lys |
| 290 | | | | | | 295 | | | | 300 | | | | | |
| Asp | Pro | Thr | Cys | Arg | Pro | Lys | Leu | Ser | Asn | Val | Val | Glu | Phe | Ser | Val |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| Pro | Leu | Asn | Gly | Cys | Gly | Thr | Ile | Arg | Lys | Val | Glu | Asp | Gln | Ser | Ile |
| | | | | 325 | | | | | 330 | | | | | 335 | |
| Thr | Tyr | Thr | Asn | Ile | Ile | Thr | Phe | Ser | Ala | Ser | Ser | Thr | Ser | Glu | Val |
| | | | 340 | | | | | 345 | | | | | 350 | | |
| Ile | Thr | Arg | Gln | Lys | Gln | Leu | Gln | Ile | Ile | Val | Lys | Cys | Glu | Met | Gly |
| | | 355 | | | | | 360 | | | | | 365 | | | |
| His | Asn | Ser | Thr | Val | Glu | Ile | Ile | Tyr | Ile | Thr | Glu | Asp | Asp | Val | Ile |
| | 370 | | | | | 375 | | | | | 380 | | | | |
| Gln | Ser | Gln | Asn | Ala | Leu | Gly | Lys | Tyr | Asn | Thr | Ser | Met | Ala | Leu | Phe |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 |
| Glu | Ser | Asn | Ser | Phe | Glu | Lys | Thr | Ile | Leu | Glu | Ser | Pro | Tyr | Tyr | Val |
| | | | | 405 | | | | | 410 | | | | | 415 | |
| Asp | Leu | Asn | Gln | Thr | Leu | Phe | Val | Gln | Val | Ser | Leu | His | Thr | Ser | Asp |
| | | 420 | | | | | | 425 | | | | | 430 | | |
| Pro | Asn | Leu | Val | Val | Phe | Leu | Asp | Thr | Cys | Arg | Ala | Ser | Pro | Thr | Ser |
| | 435 | | | | | | 440 | | | | | 445 | | | |
| Asp | Phe | Ala | Ser | Pro | Thr | Tyr | Asp | Leu | Ile | Lys | Ser | Gly | Cys | Ser | Arg |
| | 450 | | | | | 455 | | | | | 460 | | | | |
| Asp | Glu | Thr | Cys | Lys | Val | Tyr | Pro | Leu | Phe | Gly | His | Tyr | Gly | Arg | Phe |
| 465 | | | | | 470 | | | | | 475 | | | | | 480 |
| Gln | Phe | Asn | Ala | Phe | Lys | Phe | Leu | Arg | Ser | Met | Ser | Ser | Val | Tyr | Leu |
| | | | | 485 | | | | | 490 | | | | | 495 | |
| Gln | Cys | Lys | Val | Leu | Ile | Cys | Asp | Ser | Ser | Asp | His | Gln | Ser | Arg | Cys |
| | | | 500 | | | | | 505 | | | | | 510 | | |
| Asn | Gln | Gly | Cys | Val | Ser | Arg | Ser | Lys | Arg | Asp | Ile | Ser | Ser | Tyr | Lys |
| | | 515 | | | | | 520 | | | | | 525 | | | |
| Trp | Lys | Thr | Asp | Ser | Ile | Ile | Gly | Pro | Ile | Arg | Leu | Lys | Arg | Asp | Arg |
| | 530 | | | | | 535 | | | | | 540 | | | | |
| Ser | Ala | Ser | Gly | Asn | Ser | Gly | Phe | Gln | His | Glu | Thr | His | Ala | Glu | Glu |
| 545 | | | | | 550 | | | | | 555 | | | | | 560 |
| Thr | Pro | Asn | Gln | Pro | Phe | Asn | Ser | Val | His | Leu | Phe | Ser | Phe | Met | Val |

565 570 575

Leu Ala Leu Asn Val Val Thr Val Ala Thr Ile Thr Val Arg His Phe
580 585 590

Val Asn Gln Arg Ala Asp Tyr Lys Tyr Gln Lys Leu Gln Asn Tyr
595 600 605

<210> 191
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 191
tctctattcc aaactgtggc g 21

<210> 192
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 192
tttgatgacg attcgaaggt gg 22

<210> 193
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 193
ggaaggatcc ttcaccagcc ccaattaccc aaagccgcat cctgagc 47

<210> 194
<211> 2362
<212> DNA
<213> Homo sapiens

<400> 194
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cgggacatgc ggccccagga gtcccccagg ctgcggttcc cgttgctgct gttgctgttg 120
ctgctgctgc cgccgcgcgc gtgccctgcc cacagcgcca cgcgcttcga cccacctgg 180

gagtccctgg acgcccgcga gctgcccgcg tggtttgacc aggccaagtt cggcatcttc 240
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 ttataaaaaa agttttttct ttcttcaatt ataaattaac ataagtgtac tgtaacttta 2280
 caaacgtttt aattttttaa accttttttg ctcttttgta ataacactta gcttaaaaca 2340
 taaactcatt gtgcaaatgt aa 2362

<210> 195

<211> 467

<212> PRT

<213> Homo sapiens

<400> 195

Met Arg Pro Gln Glu Leu Pro Arg Leu Ala Phe Pro Leu Leu Leu Leu
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Leu Leu Leu Leu Leu Pro Pro Pro Pro Cys Pro Ala His Ser Ala Thr
 20 25 30

Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln Leu Pro Ala
 35 40 45

Trp Phe Asp Gln Ala Lys Phe Gly Ile Phe Ile His Trp Gly Val Phe
 50 55 60
 Ser Val Pro Ser Phe Gly Ser Glu Trp Phe Trp Trp Tyr Trp Gln Lys
 65 70 75 80
 Glu Lys Ile Pro Lys Tyr Val Glu Phe Met Lys Asp Asn Tyr Pro Pro
 85 90 95
 Ser Phe Lys Tyr Glu Asp Phe Gly Pro Leu Phe Thr Ala Lys Phe Phe
 100 105 110
 Asn Ala Asn Gln Trp Ala Asp Ile Phe Gln Ala Ser Gly Ala Lys Tyr
 115 120 125
 Ile Val Leu Thr Ser Lys His His Glu Gly Phe Thr Leu Trp Gly Ser
 130 135 140
 Glu Tyr Ser Trp Asn Trp Asn Ala Ile Asp Glu Gly Pro Lys Arg Asp
 145 150 155 160
 Ile Val Lys Glu Leu Glu Val Ala Ile Arg Asn Arg Thr Asp Leu Arg
 165 170 175
 Phe Gly Leu Tyr Tyr Ser Leu Phe Glu Trp Phe His Pro Leu Phe Leu
 180 185 190
 Glu Asp Glu Ser Ser Ser Phe His Lys Arg Gln Phe Pro Val Ser Lys
 195 200 205
 Thr Leu Pro Glu Leu Tyr Glu Leu Val Asn Asn Tyr Gln Pro Glu Val
 210 215 220
 Leu Trp Ser Asp Gly Asp Gly Gly Ala Pro Asp Gln Tyr Trp Asn Ser
 225 230 235 240
 Thr Gly Phe Leu Ala Trp Leu Tyr Asn Glu Ser Pro Val Arg Gly Thr
 245 250 255
 Val Val Thr Asn Asp Arg Trp Gly Ala Gly Ser Ile Cys Lys His Gly
 260 265 270
 Gly Phe Tyr Thr Cys Ser Asp Arg Tyr Asn Pro Gly His Leu Leu Pro
 275 280 285
 His Lys Trp Glu Asn Cys Met Thr Ile Asp Lys Leu Ser Trp Gly Tyr
 290 295 300
 Arg Arg Glu Ala Gly Ile Ser Asp Tyr Leu Thr Ile Glu Glu Leu Val
 305 310 315 320
 Lys Gln Leu Val Glu Thr Val Ser Cys Gly Gly Asn Leu Leu Met Asn
 325 330 335

Ile Gly Pro Thr Leu Asp Gly Thr Ile Ser Val Val Phe Glu Glu Arg
 340 345 350

Leu Arg Gln Val Gly Ser Trp Leu Lys Val Asn Gly Glu Ala Ile Tyr
 355 360 365

Glu Thr Tyr Thr Trp Arg Ser Gln Asn Asp Thr Val Thr Pro Asp Val
 370 375 380

Trp Tyr Thr Ser Lys Pro Lys Glu Lys Leu Val Tyr Ala Ile Phe Leu
 385 390 395 400

Lys Trp Pro Thr Ser Gly Gln Leu Phe Leu Gly His Pro Lys Ala Ile
 405 410 415

Leu Gly Ala Thr Glu Val Lys Leu Leu Gly His Gly Gln Pro Leu Asn
 420 425 430

Trp Ile Ser Leu Glu Gln Asn Gly Ile Met Val Glu Leu Pro Gln Leu
 435 440 445

Thr Ile His Gln Met Pro Cys Lys Trp Gly Trp Ala Leu Ala Leu Thr
 450 455 460

Asn Val Ile
 465

<210> 196

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 196

tggtttgacc aggccaagtt cgg

23

<210> 197

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 197

ggattcatcc tcaaggaaga gcgg

24

<210> 198

<211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 198
 aacttgacgc atcagccact ctgc

24

<210> 199
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 199
 ttccgtgccc agcttcggta gcgagtgggt ctggtggtat tggca

45

<210> 200
 <211> 2372
 <212> DNA
 <213> Homo sapiens

<400> 200
 agcagggaaa tccggatgtc tcggttatga agtggagcag tgagtgtgag cctcaacata 60
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 catctgaggt gtttccctgg ctctgaaggg gtaggcacga tggccagggtg cttcagcctg 180
 gtgttgcttc tcaattccat ctggaccacg aggtcctctg tccaaggctc tttgcgtgca 240
 gaagagcttt ccatccagggt gtcattgcaga attatgggga tcacccttgt gagcaaaaag 300
 gcgaaccagc agctgaattt cacagaagct aaggaggcct gtaggctgct gggactaagt 360
 ttggccggca aggaccaagt tgaacagcc ttgaaagcta gctttgaaac ttgcagctat 420
 ggctgggttg gagatggatt cgtgggtcatc tctaggatta gcccaaacc caagtgtggg 480
 aaaaatgggg tgggtgtcct gatttggag gttccagtga gccgacagtt tgcagcctat 540
 tgttacaact catctgatac ttggactaac tcgtgcattc cagaaattat caccacccaa 600
 gatcccatat tcaacactca aactgcaaca caaacaacag aatttattgt cagtgcagct 660
 acctactcgg tggcatcccc ttactctaca atacctgccc ctactactac tctcctgct 720
 ccagcttcca cttctattcc acggagaaaa aaattgattt gtgtcacaga agtttttatg 780
 gaaactagca ccatgtctac agaaactgaa ccatttgttg aaaataaagc agcattcaag 840
 aatgaagctg ctgggttttg aggtgtcccc acggctctgc tagtgcttgc tctcctcttc 900
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 tttacaaaca agaatacaga gaaggaaatg atcgaaacca aagtagtaaa ggaggagaag 1020
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gactaatctt attcattttc tctaatatgg caaccattat aaccttaatt tattattaac 2220
atacctaaga agtacattgt tacctctata taccaaagca catttttaaaa gtgccattaa 2280
caaatgtatc actagccctc ctttttccaa caagaaggga ctgagagatg cagaaatatt 2340
tgtgacaaaa aattaaagca tttagaaaaac tt 2372

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<210> 201

<211> 322

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic protein

<400> 201

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Met Ala Arg Cys Phe Ser Leu Val Leu Leu Leu Thr Ser Ile Trp Thr
  1              5              10              15

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Thr Arg Leu Leu Val Gln Gly Ser Leu Arg Ala Glu Glu Leu Ser Ile
      20              25              30

```

```

Gln Val Ser Cys Arg Ile Met Gly Ile Thr Leu Val Ser Lys Lys Ala
    35              40              45

```

```

Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu Ala Cys Arg Leu Leu
    50              55              60

```

```

Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala
    65              70              75              80

```

```

Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val
      85              90              95

```

```

Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly
    100              105              110

```

```

Val Leu Ile Trp Lys Val Pro Val Ser Arg Gln Phe Ala Ala Tyr Cys
    115              120              125

```

```

Tyr Asn Ser Ser Asp Thr Trp Thr Asn Ser Cys Ile Pro Glu Ile Ile
    130              135              140

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Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr
 145 150 155 160
 Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser
 165 170 175
 Thr Ile Pro Ala Pro Thr Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser
 180 185 190
 Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu
 195 200 205
 Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala
 210 215 220
 Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu
 225 230 235 240
 Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Ala Gly Leu Gly Phe
 245 250 255
 Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn Lys Asn
 260 265 270
 Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala
 275 280 285
 Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr Asp Lys Asn Pro
 290 295 300
 Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val Arg Cys Leu Glu Ala
 305 310 315 320
 Glu Val

<210> 202

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 202

gagctttcca tccaggtgac atgc

24

<210> 203

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 203

gtcagtgcaca gtacctactc gg

22

<210> 204

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 204

tggagcagga ggagtagtag tagg

24

<210> 205

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 205

aggaggcctg taggctgctg ggactaagtt tggccggcaa ggaccaagtt

50

<210> 206

<211> 1620

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (973)

<223> a, t, c or g

<220>

<221> modified_base

<222> (977)

<223> a, t, c or g

<220>

<221> modified_base

<222> (996)

<223> a, t, c or g

<220>

<221> modified_base

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<222> (1003)

<223> a, t, c or g

<400> 206

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acatactccc cacaccagat tgatggcttt ccgtaataaa aagattggga tttcctttt 1620

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<210> 207

<211> 296

<212> PRT

<213> Homo sapiens

<400> 207

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Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg
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Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu
 20             25             30

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly
 35             40             45

Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg
 50             55             60

Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn
 65             70             75             80

```


Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe
85 90 95

Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met
100 105 110

Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys
115 120 125

Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys
130 135 140

Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile Val
145 150 155 160

Glu Phe Phe Ala Asn Trp Ser Asn Asp Cys Gln Ser Phe Ala Pro Ile
165 170 175

Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly
180 185 190

Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val
195 200 205

Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln
210 215 220

Gly Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg
225 230 235 240

Ala Val Ser Trp Thr Phe Ser Glu Glu Asn Val Ile Arg Glu Phe Asn
245 250 255

Leu Asn Glu Leu Tyr Gln Arg Ala Lys Lys Leu Ser Lys Ala Gly Asp
260 265 270

Asn Ile Pro Glu Glu Gln Pro Val Ala Ser Thr Pro Thr Thr Val Ser
275 280 285

Asp Gly Glu Asn Lys Lys Asp Lys
290 295

<210> 208

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 208

gcttgatat tcgcatgggc ctac

<210> 209
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 209
 tggagacaat atccctgagg 20

<210> 210
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 210
 aacagttggc cacagcatgg cagg 24

<210> 211
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 211
 ccattgatga ggaactagaa cgggacaaga gggtcacttg gattgtggag 50

<210> 212
 <211> 1985
 <212> DNA
 <213> Homo sapiens

<400> 212
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<212> PRT

<213> Homo sapiens

<400> 213

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Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Leu Asn Gly Val Lys
 35 40 45

Leu Val Val Glu Thr Pro Glu Glu Thr Leu Phe Thr Tyr Gln Gly Ala
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Ser Val Ile Leu Pro Cys Arg Tyr Arg Tyr Glu Pro Ala Leu Val Ser
 65 70 75 80

Pro Arg Arg Val Arg Val Lys Trp Trp Lys Leu Ser Glu Asn Gly Ala
 85 90 95

Pro Glu Lys Asp Val Leu Val Ala Ile Gly Leu Arg His Arg Ser Phe
 100 105 110

Gly Asp Tyr Gln Gly Arg Val His Leu Arg Gln Asp Lys Glu His Asp

400 213 360 PRT Homo sapiens

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| Arg | Cys | Glu | Val | Ile | Asp | Gly | Leu | Glu | Asp | Glu | Ser | Gly | Leu | Val | Glu |
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| Leu | Glu | Leu | Arg | Gly | Val | Val | Phe | Pro | Tyr | Gln | Ser | Pro | Asn | Gly | Arg |
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| Tyr | Gln | Phe | Asn | Phe | His | Glu | Gly | Gln | Gln | Val | Cys | Ala | Glu | Gln | Ala |
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| Pro | Ile | Met | Leu | Pro | Arg | Gln | Pro | Cys | Gly | Gly | Pro | Gly | Leu | Ala | Pro |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Gly | Val | Arg | Ser | Tyr | Gly | Pro | Arg | His | Arg | Arg | Leu | His | Arg | Tyr | Asp |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Val | Phe | Cys | Phe | Ala | Thr | Ala | Leu | Lys | Gly | Arg | Val | Tyr | Tyr | Leu | Glu |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| His | Pro | Glu | Lys | Leu | Thr | Leu | Thr | Glu | Ala | Arg | Glu | Ala | Cys | Gln | Glu |
| | | 275 | | | | | 280 | | | | | 285 | | | |
| Asp | Asp | Ala | Thr | Ile | Ala | Lys | Val | Gly | Gln | Leu | Phe | Ala | Ala | Trp | Lys |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Phe | His | Gly | Leu | Asp | Arg | Cys | Asp | Ala | Gly | Trp | Leu | Ala | Asp | Gly | Ser |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| Val | Arg | Tyr | Pro | Val | Val | His | Pro | His | Pro | Asn | Cys | Gly | Pro | Pro | Glu |
| | | | | 325 | | | | | 330 | | | | | 335 | |
| Pro | Gly | Val | Arg | Ser | Phe | Gly | Phe | Pro | Asp | Pro | Gln | Ser | Arg | Leu | Tyr |
| | | | 340 | | | | | 345 | | | | | 350 | | |
| Gly | Val | Tyr | Cys | Tyr | Arg | Gln | His | | | | | | | | |
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<210> 214

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 214
tgcttgcgta ctgccctc 18

<210> 215
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 215
ttcccttggtg gggtggag 18

<210> 216
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 216
agggctggaa gccagttc 18

<210> 217
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 217
agccagtgcg gaaatgcg 18

<210> 218
<211> 24
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 218
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Sequence

<210> 219
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 <212> DNA
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<210> 220
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 <212> DNA
 <213> Homo sapiens

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 aaa 1503

<210> 221
 <211> 328
 <212> PRT
 <213> Homo sapiens

<400> 221
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| Arg Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala | 35 | 40 | 45 |
| His Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val | 50 | 55 | 60 |
| Ala Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu | 65 | 70 | 75 |
| Gly Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp | 85 | 90 | 95 |
| Val Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg | 100 | 105 | 110 |
| His Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp | 115 | 120 | 125 |
| Arg Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly | 130 | 135 | 140 |
| His Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr | 145 | 150 | 155 |
| Tyr Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp | 165 | 170 | 175 |
| Gln Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu | 180 | 185 | 190 |
| His Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr | 195 | 200 | 205 |
| Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu | 210 | 215 | 220 |
| Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Glu Pro Ala | 225 | 230 | 235 |
| Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn | 245 | 250 | 255 |
| Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro | 260 | 265 | 270 |
| Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu | 275 | 280 | 285 |

Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly
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Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp
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Leu Thr Arg His His Asp Glu Leu
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<210> 222

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 222

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<210> 223

<211> 18

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 223

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18

<210> 224

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 224

gtgcgcggtg ctcacagctc atc

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<210> 225

<211> 44

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
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44

<210> 226
 <211> 2403
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 <213> Homo sapiens

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<211> 550

<212> PRT

<213> Homo sapiens

<400> 227

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Thr Cys Phe Thr Arg Gly Leu Asp Ile Arg Lys Glu Lys Ala Asp Val
      35           40           45

Leu Cys Pro Gly Gly Cys Pro Leu Glu Glu Phe Ser Val Tyr Gly Asn
      50           55           60

Ile Val Tyr Ala Ser Val Ser Ser Ile Cys Gly Ala Ala Val His Arg
      65           70           75           80

Gly Val Ile Ser Asn Ser Gly Gly Pro Val Arg Val Tyr Ser Leu Pro
      85           90           95

Gly Arg Glu Asn Tyr Ser Ser Val Asp Ala Asn Gly Ile Gln Ser Gln
      100          105          110

Met Leu Ser Arg Trp Ser Ala Ser Phe Thr Val Thr Lys Gly Lys Ser
      115          120          125

Ser Thr Gln Glu Ala Thr Gly Gln Ala Val Ser Thr Ala His Pro Pro
      130          135          140

Thr Gly Lys Arg Leu Lys Lys Thr Pro Glu Lys Lys Thr Gly Asn Lys
      145          150          155          160

Asp Cys Lys Ala Asp Ile Ala Phe Leu Ile Asp Gly Ser Phe Asn Ile
      165          170          175

Gly Gln Arg Arg Phe Asn Leu Gln Lys Asn Phe Val Gly Lys Val Ala
      180          185          190

Leu Met Leu Gly Ile Gly Thr Glu Gly Pro His Val Gly Leu Val Gln
      195          200          205

Ala Ser Glu His Pro Lys Ile Glu Phe Tyr Leu Lys Asn Phe Thr Ser
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Ala Lys Asp Val Leu Phe Ala Ile Lys Glu Val Gly Phe Arg Gly Gly
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Asn Ser Asn Thr Gly Lys Ala Leu Lys His Thr Ala Gln Lys Phe Phe
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| | | | 260 | | | | | 265 | | | | 270 | | | |
| Phe | Ile | Asp | Gly | Trp | Pro | Ser | Asp | Asp | Ile | Glu | Glu | Ala | Gly | Ile | Val |
| | | | 275 | | | | 280 | | | | 285 | | | | |
| Ala | Arg | Glu | Phe | Gly | Val | Asn | Val | Phe | Ile | Val | Ser | Val | Ala | Lys | Pro |
| | | | 290 | | | | 295 | | | | 300 | | | | |
| Ile | Pro | Glu | Glu | Leu | Gly | Met | Val | Gln | Asp | Val | Thr | Phe | Val | Asp | Lys |
| 305 | | | | 310 | | | | | | 315 | | | 320 | | |
| Ala | Val | Cys | Arg | Asn | Asn | Gly | Phe | Phe | Ser | Tyr | His | Met | Pro | Asn | Trp |
| | | | 325 | | | | | | 330 | | | 335 | | | |
| Phe | Gly | Thr | Thr | Lys | Tyr | Val | Lys | Pro | Leu | Val | Gln | Lys | Leu | Cys | Thr |
| | | | 340 | | | | | | 345 | | | 350 | | | |
| His | Glu | Gln | Met | Met | Cys | Ser | Lys | Thr | Cys | Tyr | Asn | Ser | Val | Asn | Ile |
| | | | 355 | | | | | | 360 | | | 365 | | | |
| Ala | Phe | Leu | Ile | Asp | Gly | Ser | Ser | Ser | Val | Gly | Asp | Ser | Asn | Phe | Arg |
| | | | 370 | | | 375 | | | | | | 380 | | | |
| Leu | Met | Leu | Glu | Phe | Val | Ser | Asn | Ile | Ala | Lys | Thr | Phe | Glu | Ile | Ser |
| 385 | | | | 390 | | | | | | 395 | | | 400 | | |
| Asp | Ile | Gly | Ala | Lys | Ile | Ala | Ala | Val | Gln | Phe | Thr | Tyr | Asp | Gln | Arg |
| | | | 405 | | | | | | 410 | | | 415 | | | |
| Thr | Glu | Phe | Ser | Phe | Thr | Asp | Tyr | Ser | Thr | Lys | Glu | Asn | Val | Leu | Ala |
| | | | 420 | | | | | | 425 | | | 430 | | | |
| Val | Ile | Arg | Asn | Ile | Arg | Tyr | Met | Ser | Gly | Gly | Thr | Ala | Thr | Gly | Asp |
| | | | 435 | | | 440 | | | | | | 445 | | | |
| Ala | Ile | Ser | Phe | Thr | Val | Arg | Asn | Val | Phe | Gly | Pro | Ile | Arg | Glu | Ser |
| | | | 450 | | | 455 | | | | | | 460 | | | |
| Pro | Asn | Lys | Asn | Phe | Leu | Val | Ile | Val | Thr | Asp | Gly | Gln | Ser | Tyr | Asp |
| 465 | | | | 470 | | | | | | 475 | | | 480 | | |
| Asp | Val | Gln | Gly | Pro | Ala | Ala | Ala | Ala | His | Asp | Ala | Gly | Ile | Thr | Ile |
| | | | 485 | | | | | | 490 | | | 495 | | | |
| Phe | Ser | Val | Gly | Val | Ala | Trp | Ala | Pro | Leu | Asp | Asp | Leu | Lys | Asp | Met |
| | | | 500 | | | | | | 505 | | | 510 | | | |
| Ala | Ser | Lys | Pro | Lys | Glu | Ser | His | Ala | Phe | Phe | Thr | Arg | Glu | Phe | Thr |
| | | | 515 | | | | | | 520 | | | 525 | | | |
| Gly | Leu | Glu | Pro | Ile | Val | Ser | Asp | Val | Ile | Arg | Gly | Ile | Cys | Arg | Asp |
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<210> 228
<211> 18
<212> DNA
<213> Artificial Sequence
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<400> 228
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<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 229
ctgctgtcca caggggag 18

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 230
ccttgaaqca tactgctc 18

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<210> 231
<211> 18
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 231
gagatagcaa tttccgcc 18

<210> 232

<211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 232
 ttcctcaaga gggcagcc

18

<210> 233
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
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 oligonucleotide probe

<400> 233
 cttggcacca atgtccgaga ttcc

24

<210> 234
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 <212> DNA
 <213> Artificial Sequence

<220>
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 oligonucleotide probe

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45

<210> 235
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 <213> Homo sapiens

<400> 235
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 tgttcgcgca ggttgaggaa ctgatggagg acacgcagca caaattgcgc agcgcggtgg 360
 aagagatgga ggcagaagaa gctgctgcta aagcatcatc agaagtgaac ctggcaaact 420
 tacctcccag ctatcacaat gagaccaaca cagacacgaa ggttggaat aataccatcc 480
 atgtgcaccg agaaattcac aagataacca acaaccagac tggacaaatg gtcttttcag 540
 agacagttat cacatctgtg ggagacgaag aaggcagaag gagccacgag tgcacatcgc 600
 acgaggactg tgggcccagc atgtactgcc agtttgccag cttccagtac acctgccagc 660
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<211> 350
<212> PRT
<213> Homo sapiens
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          20              25              30
Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn
          35              40              45
Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
  50              55              60
Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
  65              70              75              80

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<210> 237

<211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 237
 ggagctgcac cccttgc 17

<210> 238
 <211> 49
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 238
 ggaggactgt gccaccatga gagactcttc aaaccaagg caaaattgg 49

<210> 239
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 239
 gcagagcggg gatgcagcgg ctg 24

<210> 240
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 240
 ttggcagctt catggagg 18

<210> 241
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 241
 cctgggcaaa aatgcaac 18

<210> 242
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 242
 ctccagctcc tggcgcacct cctc

24

<210> 243
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 243
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45

<210> 244
 <211> 3679
 <212> DNA
 <213> Homo Sapien

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 cacacataca ctttctctc cttcactgaa gactcacagt cactcactct 200
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 gaatccagga ggcggaggat gcagtcagct gagtgcaccg ctgcactcca 550
 gcctgggtga cagaatgaga ctctgtctca aacaaacaaa cacgggagga 600

| | | | | | |
|-------------|-------------|------------|------------|-------------|------|
| ggggtagata | ctgcttctct | gcaacctcct | taactctgca | tctcttctt | 650 |
| ccagggctgc | ccttgatggg | gcctggcaat | gactgagcag | gccagcccc | 700 |
| agaggacaag | gaagagaagg | catattgagg | agggcaagaa | gtgacgccc | 750 |
| gtgtagaatg | actgccctgg | gagggtggtt | ccttgggccc | tggcagggtt | 800 |
| gctgaccctt | accctgcaaa | acacaaagag | caggactcca | gactctcctt | 850 |
| gtgaatggtc | ccttgccctg | cagctccacc | atgaggcttc | tctgtggcccc | 900 |
| actcttgcta | gcttgggtgg | ctggtgccac | tgccactgtg | cccgtggtag | 950 |
| cctggcatgt | tccctgcccc | cctcagtgtg | cctgccagat | ccggccctgg | 1000 |
| tatacgcccc | gctcgtccta | ccgcgaggct | accactgtgg | actgcaatga | 1050 |
| cctattcctg | acggcagtc | ccccggcact | ccccgcaggc | acacagaccc | 1100 |
| tgctcctgca | gagcaacagc | attgtccgtg | tggaccagag | tgagctgggc | 1150 |
| tacctggcca | atctcacaga | gctggacctg | tcccagaaca | gcttttcgga | 1200 |
| tgccccgagac | tgtgatttcc | atgccctgcc | ccagctgctg | agcctgcacc | 1250 |
| tagaggagaa | ccagctgacc | cggctggagg | accacagctt | tgcagggctg | 1300 |
| gccagcctac | aggaactcta | tctcaaccac | aaccagctct | accgcatcgc | 1350 |
| ccccagggcc | ttttctggcc | tcagcaactt | gctgcggctg | cacctcaact | 1400 |
| ccaacctcct | gagggccatt | gacagccgct | ggtttgaaat | gctgccccaac | 1450 |
| ttggagatac | tcatgattgg | cggcaacaag | gtagatgcca | tcttggacat | 1500 |
| gaacttccgg | cccttgcca | acctgcgtag | cctggtgcta | gcaggcatga | 1550 |
| acctgcggga | gatctccgac | tatgccctgg | aggggctgca | aagcctggag | 1600 |
| agcctctcct | tctatgacaa | ccagctggcc | cgggtgcccc | ggcggggcact | 1650 |
| ggaacaggtg | cccggtctca | agttcctaga | cctcaacaag | aaccgctcc | 1700 |
| agcgggtagg | gccggggggac | tttgccaaca | tgctgcacct | taaggagctg | 1750 |
| ggactgaaca | acatggagga | gctggtctcc | atcgacaagt | ttgccctggt | 1800 |
| gaacctcccc | gagctgacca | agctggacat | caccaataac | ccacggctgt | 1850 |
| ccttcatcca | ccccgcgccc | ttccaccacc | tgccccagat | ggagaccctc | 1900 |
| atgctcaaca | acaacgctct | cagtgccttg | caccagcaga | cgggtggagtc | 1950 |

[illegible]

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 aataaaaata aataataaca ataaaaaaaa 3679

<210> 245

<211> 713

<212> PRT

<213> Homo Sapien

<400> 245

| | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Arg | Leu | Leu | Val | Ala | Pro | Leu | Leu | Leu | Ala | Trp | Val | Ala | Gly | 1 | 5 | 10 | 15 |
| Ala | Thr | Ala | Thr | Val | Pro | Val | Val | Pro | Trp | His | Val | Pro | Cys | Pro | 20 | 25 | 30 | |
| Pro | Gln | Cys | Ala | Cys | Gln | Ile | Arg | Pro | Trp | Tyr | Thr | Pro | Arg | Ser | 35 | 40 | 45 | |
| Ser | Tyr | Arg | Glu | Ala | Thr | Thr | Val | Asp | Cys | Asn | Asp | Leu | Phe | Leu | 50 | 55 | 60 | |
| Thr | Ala | Val | Pro | Pro | Ala | Leu | Pro | Ala | Gly | Thr | Gln | Thr | Leu | Leu | 65 | 70 | 75 | |
| Leu | Gln | Ser | Asn | Ser | Ile | Val | Arg | Val | Asp | Gln | Ser | Glu | Leu | Gly | 80 | 85 | 90 | |
| Tyr | Leu | Ala | Asn | Leu | Thr | Glu | Leu | Asp | Leu | Ser | Gln | Asn | Ser | Phe | 95 | 100 | 105 | |
| Ser | Asp | Ala | Arg | Asp | Cys | Asp | Phe | His | Ala | Leu | Pro | Gln | Leu | Leu | 110 | 115 | 120 | |
| Ser | Leu | His | Leu | Glu | Glu | Asn | Gln | Leu | Thr | Arg | Leu | Glu | Asp | His | 125 | 130 | 135 | |
| Ser | Phe | Ala | Gly | Leu | Ala | Ser | Leu | Gln | Glu | Leu | Tyr | Leu | Asn | His | 140 | 145 | 150 | |

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Gln | Leu | Tyr | Arg | Ile | Ala | Pro | Arg | Ala | Phe | Ser | Gly | Leu | Ser | 155 | 160 | 165 |
| Asn | Leu | Leu | Arg | Leu | His | Leu | Asn | Ser | Asn | Leu | Leu | Arg | Ala | Ile | 170 | 175 | 180 |
| Asp | Ser | Arg | Trp | Phe | Glu | Met | Leu | Pro | Asn | Leu | Glu | Ile | Leu | Met | 185 | 190 | 195 |
| Ile | Gly | Gly | Asn | Lys | Val | Asp | Ala | Ile | Leu | Asp | Met | Asn | Phe | Arg | 200 | 205 | 210 |
| Pro | Leu | Ala | Asn | Leu | Arg | Ser | Leu | Val | Leu | Ala | Gly | Met | Asn | Leu | 215 | 220 | 225 |
| Arg | Glu | Ile | Ser | Asp | Tyr | Ala | Leu | Glu | Gly | Leu | Gln | Ser | Leu | Glu | 230 | 235 | 240 |
| Ser | Leu | Ser | Phe | Tyr | Asp | Asn | Gln | Leu | Ala | Arg | Val | Pro | Arg | Arg | 245 | 250 | 255 |
| Ala | Leu | Glu | Gln | Val | Pro | Gly | Leu | Lys | Phe | Leu | Asp | Leu | Asn | Lys | 260 | 265 | 270 |
| Asn | Pro | Leu | Gln | Arg | Val | Gly | Pro | Gly | Asp | Phe | Ala | Asn | Met | Leu | 275 | 280 | 285 |
| His | Leu | Lys | Glu | Leu | Gly | Leu | Asn | Asn | Met | Glu | Glu | Leu | Val | Ser | 290 | 295 | 300 |
| Ile | Asp | Lys | Phe | Ala | Leu | Val | Asn | Leu | Pro | Glu | Leu | Thr | Lys | Leu | 305 | 310 | 315 |
| Asp | Ile | Thr | Asn | Asn | Pro | Arg | Leu | Ser | Phe | Ile | His | Pro | Arg | Ala | 320 | 325 | 330 |
| Phe | His | His | Leu | Pro | Gln | Met | Glu | Thr | Leu | Met | Leu | Asn | Asn | Asn | 335 | 340 | 345 |
| Ala | Leu | Ser | Ala | Leu | His | Gln | Gln | Thr | Val | Glu | Ser | Leu | Pro | Asn | 350 | 355 | 360 |
| Leu | Gln | Glu | Val | Gly | Leu | His | Gly | Asn | Pro | Ile | Arg | Cys | Asp | Cys | 365 | 370 | 375 |
| Val | Ile | Arg | Trp | Ala | Asn | Ala | Thr | Gly | Thr | Arg | Val | Arg | Phe | Ile | 380 | 385 | 390 |
| Glu | Pro | Gln | Ser | Thr | Leu | Cys | Ala | Glu | Pro | Pro | Asp | Leu | Gln | Arg | 395 | 400 | 405 |
| Leu | Pro | Val | Arg | Glu | Val | Pro | Phe | Arg | Glu | Met | Thr | Asp | His | Cys | | | |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|------------|-----|-----|-----|-----|------------|-----|-----|-----|-----|------------|
| | | | | 410 | | | | | 415 | | | | | 420 |
| Leu | Pro | Leu | Ile | Ser 425 | Pro | Arg | Ser | Phe | Pro 430 | Pro | Ser | Leu | Gln | Val 435 |
| Ala | Ser | Gly | Glu | Ser 440 | Met | Val | Leu | His | Cys 445 | Arg | Ala | Leu | Ala | Glu 450 |
| Pro | Glu | Pro | Glu | Ile 455 | Tyr | Trp | Val | Thr | Pro 460 | Ala | Gly | Leu | Arg | Leu 465 |
| Thr | Pro | Ala | His | Ala 470 | Gly | Arg | Arg | Tyr | Arg 475 | Val | Tyr | Pro | Glu | Gly 480 |
| Thr | Leu | Glu | Leu | Arg 485 | Arg | Val | Thr | Ala | Glu 490 | Glu | Ala | Gly | Leu | Tyr 495 |
| Thr | Cys | Val | Ala | Gln 500 | Asn | Leu | Val | Gly | Ala 505 | Asp | Thr | Lys | Thr | Val 510 |
| Ser | Val | Val | Val | Gly 515 | Arg | Ala | Leu | Leu | Gln 520 | Pro | Gly | Arg | Asp | Glu 525 |
| Gly | Gln | Gly | Leu | Glu 530 | Leu | Arg | Val | Gln | Glu 535 | Thr | His | Pro | Tyr | His 540 |
| Ile | Leu | Leu | Ser | Trp 545 | Val | Thr | Pro | Pro | Asn 550 | Thr | Val | Ser | Thr | Asn 555 |
| Leu | Thr | Trp | Ser | Ser 560 | Ala | Ser | Ser | Leu | Arg 565 | Gly | Gln | Gly | Ala | Thr 570 |
| Ala | Leu | Ala | Arg | Leu 575 | Pro | Arg | Gly | Thr | His 580 | Ser | Tyr | Asn | Ile | Thr 585 |
| Arg | Leu | Leu | Gln | Ala 590 | Thr | Glu | Tyr | Trp | Ala 595 | Cys | Leu | Gln | Val | Ala 600 |
| Phe | Ala | Asp | Ala | His 605 | Thr | Gln | Leu | Ala | Cys 610 | Val | Trp | Ala | Arg | Thr 615 |
| Lys | Glu | Ala | Thr | Ser 620 | Cys | His | Arg | Ala | Leu 625 | Gly | Asp | Arg | Pro | Gly 630 |
| Leu | Ile | Ala | Ile | Leu 635 | Ala | Leu | Ala | Val | Leu 640 | Leu | Leu | Ala | Ala | Gly 645 |
| Leu | Ala | Ala | His | Leu 650 | Gly | Thr | Gly | Gln | Pro 655 | Arg | Lys | Gly | Val | Gly 660 |
| Gly | Arg | Arg | Pro | Leu 665 | Pro | Pro | Ala | Trp | Ala 670 | Phe | Trp | Gly | Trp | Ser 675 |

Ala Pro Ser Val Arg Val Val Ser Ala Pro Leu Val Leu Pro Trp
 680 685 690

Asn Pro Gly Arg Lys Leu Pro Arg Ser Ser Glu Gly Glu Thr Leu
 695 700 705

Leu Pro Pro Leu Ser Gln Asn Ser
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<211> 22

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<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 246

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<210> 247

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 247

aaacttgatc atggagacca gctc 24

<210> 248

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 248

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<210> 249

<211> 3401

<212> DNA

<213> Homo Sapien

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[illegible]

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a 3401

<210> 250

<211> 546

<212> PRT

<213> Homo Sapien

<400> 250

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Gln | Thr | Ile | Ile | Lys | Val | Ile | Lys | Phe | Ile | Leu | Ile | Ile |
| 1 | | | | 5 | | | | | 10 | | | | | 15 |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Tyr | Thr | Val | Tyr | Tyr | Val | His | Asn | Ile | Lys | Phe | Asp | Val | Asp |
| | | | | 20 | | | | | 25 | | | | | 30 |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Thr | Val | Asp | Ile | Glu | Ser | Leu | Thr | Gly | Tyr | Arg | Thr | Tyr | Arg |
| | | | | 35 | | | | | 40 | | | | | 45 |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Ala | His | Pro | Leu | Ala | Thr | Leu | Phe | Lys | Ile | Leu | Ala | Ser | Phe |
| | | | | 50 | | | | | 55 | | | | | 60 |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Ile | Ser | Leu | Val | Ile | Phe | Tyr | Gly | Leu | Ile | Cys | Met | Tyr | Thr |
| | | | | 65 | | | | | 70 | | | | | 75 |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Trp | Trp | Met | Leu | Arg | Arg | Ser | Leu | Lys | Lys | Tyr | Ser | Phe | Glu |
| | | | | 80 | | | | | 85 | | | | | 90 |

Ser Ile Arg Glu Glu Ser Ser Tyr Ser Asp Ile Pro Asp Val Lys

| | | | | | |
|---|-----|--|-----|--|-----|
| | 95 | | 100 | | 105 |
| Asn Asp Phe Ala Phe Met Leu His Leu Ile Asp Gln Tyr Asp Pro | 110 | | 115 | | 120 |
| Leu Tyr Ser Lys Arg Phe Ala Val Phe Leu Ser Glu Val Ser Glu | 125 | | 130 | | 135 |
| Asn Lys Leu Arg Gln Leu Asn Leu Asn Asn Glu Trp Thr Leu Asp | 140 | | 145 | | 150 |
| Lys Leu Arg Gln Arg Leu Thr Lys Asn Ala Gln Asp Lys Leu Glu | 155 | | 160 | | 165 |
| Leu His Leu Phe Met Leu Ser Gly Ile Pro Asp Thr Val Phe Asp | 170 | | 175 | | 180 |
| Leu Val Glu Leu Glu Val Leu Lys Leu Glu Leu Ile Pro Asp Val | 185 | | 190 | | 195 |
| Thr Ile Pro Pro Ser Ile Ala Gln Leu Thr Gly Leu Lys Glu Leu | 200 | | 205 | | 210 |
| Trp Leu Tyr His Thr Ala Ala Lys Ile Glu Ala Pro Ala Leu Ala | 215 | | 220 | | 225 |
| Phe Leu Arg Glu Asn Leu Arg Ala Leu His Ile Lys Phe Thr Asp | 230 | | 235 | | 240 |
| Ile Lys Glu Ile Pro Leu Trp Ile Tyr Ser Leu Lys Thr Leu Glu | 245 | | 250 | | 255 |
| Glu Leu His Leu Thr Gly Asn Leu Ser Ala Glu Asn Asn Arg Tyr | 260 | | 265 | | 270 |
| Ile Val Ile Asp Gly Leu Arg Glu Leu Lys Arg Leu Lys Val Leu | 275 | | 280 | | 285 |
| Arg Leu Lys Ser Asn Leu Ser Lys Leu Pro Gln Val Val Thr Asp | 290 | | 295 | | 300 |
| Val Gly Val His Leu Gln Lys Leu Ser Ile Asn Asn Glu Gly Thr | 305 | | 310 | | 315 |
| Lys Leu Ile Val Leu Asn Ser Leu Lys Lys Met Ala Asn Leu Thr | 320 | | 325 | | 330 |
| Glu Leu Glu Leu Ile Arg Cys Asp Leu Glu Arg Ile Pro His Ser | 335 | | 340 | | 345 |
| Ile Phe Ser Leu His Asn Leu Gln Glu Ile Asp Leu Lys Asp Asn | 350 | | 355 | | 360 |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Leu | Lys | Thr | Ile | Glu | Glu | Ile | Ile | Ser | Phe | Gln | His | Leu | His |
| | | | | 365 | | | | | 370 | | | | | 375 |
| Arg | Leu | Thr | Cys | Leu | Lys | Leu | Trp | Tyr | Asn | His | Ile | Ala | Tyr | Ile |
| | | | | 380 | | | | | 385 | | | | | 390 |
| Pro | Ile | Gln | Ile | Gly | Asn | Leu | Thr | Asn | Leu | Glu | Arg | Leu | Tyr | Leu |
| | | | | 395 | | | | | 400 | | | | | 405 |
| Asn | Arg | Asn | Lys | Ile | Glu | Lys | Ile | Pro | Thr | Gln | Leu | Phe | Tyr | Cys |
| | | | | 410 | | | | | 415 | | | | | 420 |
| Arg | Lys | Leu | Arg | Tyr | Leu | Asp | Leu | Ser | His | Asn | Asn | Leu | Thr | Phe |
| | | | | 425 | | | | | 430 | | | | | 435 |
| Leu | Pro | Ala | Asp | Ile | Gly | Leu | Leu | Gln | Asn | Leu | Gln | Asn | Leu | Ala |
| | | | | 440 | | | | | 445 | | | | | 450 |
| Ile | Thr | Ala | Asn | Arg | Ile | Glu | Thr | Leu | Pro | Pro | Glu | Leu | Phe | Gln |
| | | | | 455 | | | | | 460 | | | | | 465 |
| Cys | Arg | Lys | Leu | Arg | Ala | Leu | His | Leu | Gly | Asn | Asn | Val | Leu | Gln |
| | | | | 470 | | | | | 475 | | | | | 480 |
| Ser | Leu | Pro | Ser | Arg | Val | Gly | Glu | Leu | Thr | Asn | Leu | Thr | Gln | Ile |
| | | | | 485 | | | | | 490 | | | | | 495 |
| Glu | Leu | Arg | Gly | Asn | Arg | Leu | Glu | Cys | Leu | Pro | Val | Glu | Leu | Gly |
| | | | | 500 | | | | | 505 | | | | | 510 |
| Glu | Cys | Pro | Leu | Leu | Lys | Arg | Ser | Gly | Leu | Val | Val | Glu | Glu | Asp |
| | | | | 515 | | | | | 520 | | | | | 525 |
| Leu | Phe | Asn | Thr | Leu | Pro | Pro | Glu | Val | Lys | Glu | Arg | Leu | Trp | Arg |
| | | | | 530 | | | | | 535 | | | | | 540 |
| Ala | Asp | Lys | Glu | Gln | Ala | | | | | | | | | |
| | | | | 545 | | | | | | | | | | |

<210> 251

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 251

caacaatgag ggcaccaagc 20

<210> 252

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 252

gatggctagg ttctggaggt tctg 24

<210> 253

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 253

caacctgcag gagattgacc tcaaggacaa caacctcaag accatcg 47

<210> 254

<211> 1650

<212> DNA

<213> Homo Sapien

<400> 254

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 gcgctctccc gtcccgcggg ggttgctgct gctgccgctg ctgctggggc 100
 tgaacgcagg agctgtcatt gactggccca cagaggaggg caaggaagta 150
 tgggattatg tgacgggtccg caaggatgcc tacatgttct ggtggctcta 200
 ttatgccacc aactcctgca agaacttctc agaactgccc ctgggtcatgt 250
 ggcttcaggg cgggtccaggc ggttctagca ctggatttgg aaactttgag 300
 gaaattgggc cccttgacag tgatctcaaa ccacggaaaa ccacctggct 350
 ccaggctgcc agtctcctat ttgtggataa tcccgtgggc actgggttca 400
 gttatgtgaa tggtagtggg gcctatgcca aggacctggc tatggtggct 450
 tcagacatga tggttctcct gaagaccttc ttcagttgcc acaaagaatt 500
 ccagacagtt ccattctaca ttttctcaga gtcctatgga ggaaaaatgg 550
 cagctggcat tggcttagag ctttataagg ccattcagcg agggaccatc 600
 aagtgcaact ttgcgggggt tgccttgggt gattcctgga tctcccctgt 650
 tgattcgggt ctctcctggg gaccttacct gtacagcatg tctcttctcg 700

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gccgtaaata agggggtcta cagagaggcc acagagctgt gggggaaagc 800
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taactaaaag cactcccacg tctacaatgg agtcgagtct agaattcaca 900
cagagccacc tagtttgtct ttgtcagcgc cacgtgagac acctacaacg 950
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gctggaggca gggatcaacg tgacggtgta taatggacag ctggatctca 1150
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gatcaagaag gttctgacca gcttctgcag aggataaaat cattgtctct 1550
ggaggcaatt tggaaattat ttctgcttct taaaaaaacc taagattttt 1600
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<210> 255

<211> 452

<212> PRT

<213> Homo Sapien

<400> 255

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Leu | Ala | Leu | Arg | Arg | Ser | Pro | Val | Pro | Arg | Trp | Leu | Leu |
| 1 | | | | 5 | | | | | 10 | | | | 15 | |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Leu | Pro | Leu | Leu | Leu | Gly | Leu | Asn | Ala | Gly | Ala | Val | Ile | Asp |
| | | | 20 | | | | | 25 | | | | | 30 | |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Pro | Thr | Glu | Glu | Gly | Lys | Glu | Val | Trp | Asp | Tyr | Val | Thr | Val |
| | | | 35 | | | | | 40 | | | | | 45 | |

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Lys | Asp | Ala | Tyr | Met | Phe | Trp | Trp | Leu | Tyr | Tyr | Ala | Thr | Asn | 50 | 55 | 60 |
| Ser | Cys | Lys | Asn | Phe | Ser | Glu | Leu | Pro | Leu | Val | Met | Trp | Leu | Gln | 65 | 70 | 75 |
| Gly | Gly | Pro | Gly | Gly | Ser | Ser | Thr | Gly | Phe | Gly | Asn | Phe | Glu | Glu | 80 | 85 | 90 |
| Ile | Gly | Pro | Leu | Asp | Ser | Asp | Leu | Lys | Pro | Arg | Lys | Thr | Thr | Trp | 95 | 100 | 105 |
| Leu | Gln | Ala | Ala | Ser | Leu | Leu | Phe | Val | Asp | Asn | Pro | Val | Gly | Thr | 110 | 115 | 120 |
| Gly | Phe | Ser | Tyr | Val | Asn | Gly | Ser | Gly | Ala | Tyr | Ala | Lys | Asp | Leu | 125 | 130 | 135 |
| Ala | Met | Val | Ala | Ser | Asp | Met | Met | Val | Leu | Leu | Lys | Thr | Phe | Phe | 140 | 145 | 150 |
| Ser | Cys | His | Lys | Glu | Phe | Gln | Thr | Val | Pro | Phe | Tyr | Ile | Phe | Ser | 155 | 160 | 165 |
| Glu | Ser | Tyr | Gly | Gly | Lys | Met | Ala | Ala | Gly | Ile | Gly | Leu | Glu | Leu | 170 | 175 | 180 |
| Tyr | Lys | Ala | Ile | Gln | Arg | Gly | Thr | Ile | Lys | Cys | Asn | Phe | Ala | Gly | 185 | 190 | 195 |
| Val | Ala | Leu | Gly | Asp | Ser | Trp | Ile | Ser | Pro | Val | Asp | Ser | Val | Leu | 200 | 205 | 210 |
| Ser | Trp | Gly | Pro | Tyr | Leu | Tyr | Ser | Met | Ser | Leu | Leu | Glu | Asp | Lys | 215 | 220 | 225 |
| Gly | Leu | Ala | Glu | Val | Ser | Lys | Val | Ala | Glu | Gln | Val | Leu | Asn | Ala | 230 | 235 | 240 |
| Val | Asn | Lys | Gly | Leu | Tyr | Arg | Glu | Ala | Thr | Glu | Leu | Trp | Gly | Lys | 245 | 250 | 255 |
| Ala | Glu | Met | Ile | Ile | Glu | Gln | Asn | Thr | Asp | Gly | Val | Asn | Phe | Tyr | 260 | 265 | 270 |
| Asn | Ile | Leu | Thr | Lys | Ser | Thr | Pro | Thr | Ser | Thr | Met | Glu | Ser | Ser | 275 | 280 | 285 |
| Leu | Glu | Phe | Thr | Gln | Ser | His | Leu | Val | Cys | Leu | Cys | Gln | Arg | His | 290 | 295 | 300 |
| Val | Arg | His | Leu | Gln | Arg | Asp | Ala | Leu | Ser | Gln | Leu | Met | Asn | Gly | | | |

| | | |
|-------------------------------------|-------------------------|-----|
| 305 | 310 | 315 |
| Pro Ile Arg Lys Lys Leu Lys Ile Ile | Pro Glu Asp Gln Ser Trp | |
| 320 | 325 | 330 |
| Gly Gly Gln Ala Thr Asn Val Phe Val | Asn Met Glu Glu Asp Phe | |
| 335 | 340 | 345 |
| Met Lys Pro Val Ile Ser Ile Val Asp | Glu Leu Leu Glu Ala Gly | |
| 350 | 355 | 360 |
| Ile Asn Val Thr Val Tyr Asn Gly Gln | Leu Asp Leu Ile Val Asp | |
| 365 | 370 | 375 |
| Thr Met Gly Gln Glu Ala Trp Val Arg | Lys Leu Lys Trp Pro Glu | |
| 380 | 385 | 390 |
| Leu Pro Lys Phe Ser Gln Leu Lys Trp | Lys Ala Leu Tyr Ser Asp | |
| 395 | 400 | 405 |
| Pro Lys Ser Leu Glu Thr Ser Ala Phe | Val Lys Ser Tyr Lys Asn | |
| 410 | 415 | 420 |
| Leu Ala Phe Tyr Trp Ile Leu Lys Ala | Gly His Met Val Pro Ser | |
| 425 | 430 | 435 |
| Asp Gln Gly Asp Met Ala Leu Lys Met | Met Arg Leu Val Thr Gln | |
| 440 | 445 | 450 |

Gln Glu

<210> 256

<211> 1100

<212> DNA

<213> Homo Sapien

<400> 256

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ccgttatcag gaccatgcgg ccgacgggtc atcacgtcgc gcatcgtggg 150
tggagaggac gccgaactcg ggcgttgccc gtggcagggg agcctgcgcc 200
tgtgggattc ccacgtatgc ggagtgagcc tgctcagcca ccgctgggca 250
ctcacggcgg cgcactgctt tgaaacctat agtgacctta gtgatccctc 300
cgggtggatg gtccagtttg gccagctgac ttccatgcc a tccttctgga 350
gcctgcaggc ctactacacc cgttacttcg tatcgaatat ctatctgagc 400

```



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<210> 257
<211> 314
<212> PRT
<213> Homo Sapien
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<400> 257
Met Gly Ala Arg Gly Ala Leu Leu Leu Ala Leu Leu Leu Ala Arg
 1          5          10          15

Ala Gly Leu Arg Lys Pro Glu Ser Gln Glu Ala Ala Pro Leu Ser
          20          25          30

Gly Pro Cys Gly Arg Arg Val Ile Thr Ser Arg Ile Val Gly Gly
          35          40          45

Glu Asp Ala Glu Leu Gly Arg Trp Pro Trp Gln Gly Ser Leu Arg
          50          55          60

Leu Trp Asp Ser His Val Cys Gly Val Ser Leu Leu Ser His Arg
          65          70          75

Trp Ala Leu Thr Ala Ala His Cys Phe Glu Thr Tyr Ser Asp Leu
          80          85          90

```

Ser Asp Pro Ser Gly Trp Met Val Gln Phe Gly Gln Leu Thr Ser
 95 100 105
 Met Pro Ser Phe Trp Ser Leu Gln Ala Tyr Tyr Thr Arg Tyr Phe
 110 115 120
 Val Ser Asn Ile Tyr Leu Ser Pro Arg Tyr Leu Gly Asn Ser Pro
 125 130 135
 Tyr Asp Ile Ala Leu Val Lys Leu Ser Ala Pro Val Thr Tyr Thr
 140 145 150
 Lys His Ile Gln Pro Ile Cys Leu Gln Ala Ser Thr Phe Glu Phe
 155 160 165
 Glu Asn Arg Thr Asp Cys Trp Val Thr Gly Trp Gly Tyr Ile Lys
 170 175 180
 Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu Gln Glu Val Gln
 185 190 195
 Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu Phe Leu Lys
 200 205 210
 Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys Ala Gly
 215 220 225
 Asn Ala Gln Gly Gly Lys Asp Ala Cys Phe Gly Asp Ser Gly Gly
 230 235 240
 Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val
 245 250 255
 Val Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val
 260 265 270
 Tyr Thr Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met
 275 280 285
 Ala Gln Ser Gly Met Ser Gln Pro Asp Pro Ser Trp Pro Leu Leu
 290 295 300
 Phe Phe Pro Leu Leu Trp Ala Leu Pro Leu Leu Gly Pro Val
 305 310

<210> 258

<211> 2427

<212> DNA

<213> Homo Sapien

<400> 258

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 gaacctcggc ctctactcca gtgtttgggg ggatcctatc cttgatcaat 1500
 gagcacagga tccttagtgg ccgccccctt cttggctttc tcaacccaag 1550
 gctctaccag cagcatgggg caggtctctt tgatgtaacc cgtggctgcc 1600
 atgagtcctg tctggatgaa gaggtagagg gccagggttt ctgctctggt 1650
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 agccctgctg aacctcaac tattgactgc tgcagacagc ttatctccct 1850
 aacctgaaa tgctgtgagc ttgacttgac tcccaaccct accatgctcc 1900
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 gtaactagca ttttttgaat gcctctccct ccgcatctca tctttctctt 2000
 ttcaatcagg cttttccaaa gggttgtata cagactctgt gcactatttc 2050
 acttgatatt cattccccaa ttcactgcaa ggagacctct actgtcaccg 2100
 tttactcttt cctaccctga catccagaaa caatggcctc cagtgcatac 2150
 ttctcaatct ttgctttatg gcctttccat catagttgcc cactccctct 2200
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 tctcatcaat ttctgcttct tcatggaatg ctgaccttca ttgctccatt 2300
 tgtagatttt tgctcttctc agtttactca ttgtccccctg gaacaaatca 2350
 ctgacatcta caaccattac catctcacta aataagactt tctatccaat 2400
 aatgattgat acctcaaagt taaaaaa 2427

<210> 259

<211> 556

<212> PRT

<213> Homo Sapien

<400> 259

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Leu | Gln | Ala | Cys | Leu | Leu | Gly | Leu | Phe | Ala | Leu | Ile | Leu |
| 1 | | | | | 5 | | | | 10 | | | | 15 | |

Ser Gly Lys Cys Ser Tyr Ser Pro Glu Pro Asp Gln Arg Arg Thr

| | | | | | |
|---|-----|--|-----|--|-----|
| | 20 | | 25 | | 30 |
| Leu Pro Pro Gly Trp Val Ser Leu Gly Arg Ala Asp Pro Glu Glu | 35 | | 40 | | 45 |
| Glu Leu Ser Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg | 50 | | 55 | | 60 |
| Leu Ser Glu Leu Val Gln Ala Val Ser Asp Pro Ser Ser Pro Gln | 65 | | 70 | | 75 |
| Tyr Gly Lys Tyr Leu Thr Leu Glu Asn Val Ala Asp Leu Val Arg | 80 | | 85 | | 90 |
| Pro Ser Pro Leu Thr Leu His Thr Val Gln Lys Trp Leu Leu Ala | 95 | | 100 | | 105 |
| Ala Gly Ala Gln Lys Cys His Ser Val Ile Thr Gln Asp Phe Leu | 110 | | 115 | | 120 |
| Thr Cys Trp Leu Ser Ile Arg Gln Ala Glu Leu Leu Leu Pro Gly | 125 | | 130 | | 135 |
| Ala Glu Phe His His Tyr Val Gly Gly Pro Thr Glu Thr His Val | 140 | | 145 | | 150 |
| Val Arg Ser Pro His Pro Tyr Gln Leu Pro Gln Ala Leu Ala Pro | 155 | | 160 | | 165 |
| His Val Asp Phe Val Gly Gly Leu His Arg Phe Pro Pro Thr Ser | 170 | | 175 | | 180 |
| Ser Leu Arg Gln Arg Pro Glu Pro Gln Val Thr Gly Thr Val Gly | 185 | | 190 | | 195 |
| Leu His Leu Gly Val Thr Pro Ser Val Ile Arg Lys Arg Tyr Asn | 200 | | 205 | | 210 |
| Leu Thr Ser Gln Asp Val Gly Ser Gly Thr Ser Asn Asn Ser Gln | 215 | | 220 | | 225 |
| Ala Cys Ala Gln Phe Leu Glu Gln Tyr Phe His Asp Ser Asp Leu | 230 | | 235 | | 240 |
| Ala Gln Phe Met Arg Leu Phe Gly Gly Asn Phe Ala His Gln Ala | 245 | | 250 | | 255 |
| Ser Val Ala Arg Val Val Gly Gln Gln Gly Arg Gly Arg Ala Gly | 260 | | 265 | | 270 |
| Ile Glu Ala Ser Leu Asp Val Gln Tyr Leu Met Ser Ala Gly Ala | 275 | | 280 | | 285 |

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Ile | Ser | Thr | Trp | Val | Tyr | Ser | Ser | Pro | Gly | Arg | His | Glu | Gly | 290 | 295 | 300 |
| Gln | Glu | Pro | Phe | Leu | Gln | Trp | Leu | Met | Leu | Leu | Ser | Asn | Glu | Ser | 305 | 310 | 315 |
| Ala | Leu | Pro | His | Val | His | Thr | Val | Ser | Tyr | Gly | Asp | Asp | Glu | Asp | 320 | 325 | 330 |
| Ser | Leu | Ser | Ser | Ala | Tyr | Ile | Gln | Arg | Val | Asn | Thr | Glu | Leu | Met | 335 | 340 | 345 |
| Lys | Ala | Ala | Ala | Arg | Gly | Leu | Thr | Leu | Leu | Phe | Ala | Ser | Gly | Asp | 350 | 355 | 360 |
| Ser | Gly | Ala | Gly | Cys | Trp | Ser | Val | Ser | Gly | Arg | His | Gln | Phe | Arg | 365 | 370 | 375 |
| Pro | Thr | Phe | Pro | Ala | Ser | Ser | Pro | Tyr | Val | Thr | Thr | Val | Gly | Gly | 380 | 385 | 390 |
| Thr | Ser | Phe | Gln | Glu | Pro | Phe | Leu | Ile | Thr | Asn | Glu | Ile | Val | Asp | 395 | 400 | 405 |
| Tyr | Ile | Ser | Gly | Gly | Gly | Phe | Ser | Asn | Val | Phe | Pro | Arg | Pro | Ser | 410 | 415 | 420 |
| Tyr | Gln | Glu | Glu | Ala | Val | Thr | Lys | Phe | Leu | Ser | Ser | Ser | Pro | His | 425 | 430 | 435 |
| Leu | Pro | Pro | Ser | Ser | Tyr | Phe | Asn | Ala | Ser | Gly | Arg | Ala | Tyr | Pro | 440 | 445 | 450 |
| Asp | Val | Ala | Ala | Leu | Ser | Asp | Gly | Tyr | Trp | Val | Val | Ser | Asn | Arg | 455 | 460 | 465 |
| Val | Pro | Ile | Pro | Trp | Val | Ser | Gly | Thr | Ser | Ala | Ser | Thr | Pro | Val | 470 | 475 | 480 |
| Phe | Gly | Gly | Ile | Leu | Ser | Leu | Ile | Asn | Glu | His | Arg | Ile | Leu | Ser | 485 | 490 | 495 |
| Gly | Arg | Pro | Pro | Leu | Gly | Phe | Leu | Asn | Pro | Arg | Leu | Tyr | Gln | Gln | 500 | 505 | 510 |
| His | Gly | Ala | Gly | Leu | Phe | Asp | Val | Thr | Arg | Gly | Cys | His | Glu | Ser | 515 | 520 | 525 |
| Cys | Leu | Asp | Glu | Glu | Val | Glu | Gly | Gln | Gly | Phe | Cys | Ser | Gly | Pro | 530 | 535 | 540 |
| Gly | Trp | Asp | Pro | Val | Thr | Gly | Trp | Gly | Thr | Pro | Thr | Ser | Gln | Leu | 545 | 550 | 555 |

Cys

<210> 260

<211> 1638

<212> DNA

<213> Homo Sapien

<400> 260

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agtgagccct tacagtgcc cctggaaacc cacttggcct gcataccgcc 200
tccttgtcgt cttgccccag tctaccctca atttagccaa gccagacttt 250
ggagccgaag ccaaattaga agtatcttct tcatgtggac ccagtggtca 300
taagggaact cactgcccc cttacgaaga ggccaagcaa tatctgtctt 350
atgaaacgct ctatgccaat ggcagccgca cagagacgca ggtgggcatc 400
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gtgaagttaa ccacgggctg caccggcacc ctggtggcag agaagcatgt 600
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aagccccaca agagaaaatt tatgaagatt ggggtgagcc ctctgctaa 900
gcagctgcca gggggcagaa ttcacttctc tggttatgac aatgaccgac 950
caggcaattt ggtgtatcgc ttctgtgacg tcaaagacga gacctatgac 1000
ttgtcttacc agcaatgcga tgcccagcca ggggccagcg ggtctggggt 1050
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ttggcatttt ttcagggcac cagtgggtgg acatgaatgg ttccccacag 1150
 gatttcaacg tggctgtcag aatcactcct ctcaaatatg cccagatttg 1200
 ctattggatt aaaggaaact acctggattg tagggagggg tgacacagtg 1250
 ttccctcctg gcagcaatta agggctcttca tgttcttatt ttaggagagg 1300
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 tgtgtgtaag gtgtcttata atcttttacc tatttcttac aattgcaaga 1400
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 ttttaagcagt ttgaaggcat acttttgcac agaaataaaa aaaataactga 1500
 tttggggcaa tgaggaatat ttgacaatta agttaatctt cacgtttttg 1550
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<210> 261

<211> 383

<212> PRT

<213> Homo Sapien

<400> 261

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Gly | Ile | Pro | Gly | Leu | Leu | Phe | Leu | Leu | Phe | Phe | Leu | Leu |
| 1 | | | | 5 | | | | 10 | | | | | 15 | |
| Cys | Ala | Val | Gly | Gln | Val | Ser | Pro | Tyr | Ser | Ala | Pro | Trp | Lys | Pro |
| | | | | 20 | | | | 25 | | | | | 30 | |
| Thr | Trp | Pro | Ala | Tyr | Arg | Leu | Pro | Val | Val | Leu | Pro | Gln | Ser | Thr |
| | | | | 35 | | | | 40 | | | | | 45 | |
| Leu | Asn | Leu | Ala | Lys | Pro | Asp | Phe | Gly | Ala | Glu | Ala | Lys | Leu | Glu |
| | | | | 50 | | | | 55 | | | | | 60 | |
| Val | Ser | Ser | Ser | Cys | Gly | Pro | Gln | Cys | His | Lys | Gly | Thr | Pro | Leu |
| | | | | 65 | | | | 70 | | | | | 75 | |
| Pro | Thr | Tyr | Glu | Glu | Ala | Lys | Gln | Tyr | Leu | Ser | Tyr | Glu | Thr | Leu |
| | | | | 80 | | | | 85 | | | | | 90 | |
| Tyr | Ala | Asn | Gly | Ser | Arg | Thr | Glu | Thr | Gln | Val | Gly | Ile | Tyr | Ile |
| | | | | 95 | | | | 100 | | | | | 105 | |
| Leu | Ser | Ser | Ser | Gly | Asp | Gly | Ala | Gln | His | Arg | Asp | Ser | Gly | Ser |
| | | | | 110 | | | | 115 | | | | | 120 | |

| | | | |
|---|-----|-----|-----|
| Ser Gly Lys Ser Arg Arg Lys Arg Gln Ile Tyr Gly Tyr Asp Ser | 125 | 130 | 135 |
| Arg Phe Ser Ile Phe Gly Lys Asp Phe Leu Leu Asn Tyr Pro Phe | 140 | 145 | 150 |
| Ser Thr Ser Val Lys Leu Ser Thr Gly Cys Thr Gly Thr Leu Val | 155 | 160 | 165 |
| Ala Glu Lys His Val Leu Thr Ala Ala His Cys Ile His Asp Gly | 170 | 175 | 180 |
| Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val Gly Phe Leu | 185 | 190 | 195 |
| Lys Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp Ser Thr | 200 | 205 | 210 |
| Ser Ala Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val Lys | 215 | 220 | 225 |
| Arg Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp | 230 | 235 | 240 |
| Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro | 245 | 250 | 255 |
| His Lys Arg Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys | 260 | 265 | 270 |
| Gln Leu Pro Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp | 275 | 280 | 285 |
| Arg Pro Gly Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu | 290 | 295 | 300 |
| Thr Tyr Asp Leu Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala | 305 | 310 | 315 |
| Ser Gly Ser Gly Val Tyr Val Arg Met Trp Lys Arg Gln Gln Gln | 320 | 325 | 330 |
| Lys Trp Glu Arg Lys Ile Ile Gly Ile Phe Ser Gly His Gln Trp | 335 | 340 | 345 |
| Val Asp Met Asn Gly Ser Pro Gln Asp Phe Asn Val Ala Val Arg | 350 | 355 | 360 |
| Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Tyr Trp Ile Lys Gly | 365 | 370 | 375 |
| Asn Tyr Leu Asp Cys Arg Glu Gly | 380 | | |

<210> 262
 <211> 1378
 <212> DNA
 <213> Homo Sapien

<400> 262
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 caggatacct gttccccag cctgtgggaa gccccagcag ctgaaccggg 200
 ttgtgggcgg cgaggacagc actgacagcg agtggccctg gatcgtgagc 250
 atccagaaga atgggaccca ccaactgcgca ggttctctgc tcaccagccg 300
 ctgggtgatc actgctgccc actgtttcaa ggacaacctg aacaaacct 350
 acctgtttct tgtgctgctg ggggcctggc agctggggaa cctgggtct 400
 cgggtccaga aggtgggtgt tgctgggtg gagccccacc ctgtgtattc 450
 ctggaaggaa ggtgcctgtg cagacattgc cctggtgcgt ctgcagcgct 500
 ccatacagtt ctgagagcgg gtctgccc tctgcctacc tgatgcctct 550
 atccacctcc ctccaaacac ccaactgctg atctcaggct gggggagcat 600
 ccaagatgga gttcccttgc cccaccctca gaccctgcag aagctgaagg 650
 ttctatcat cgactcggaa gtctgcagcc atctgtactg gcggggagca 700
 ggacagggac ccatcaactga ggacatgctg tgtgccggct acttgagggg 750
 ggagcgggat gcttgtctgg gcgactccgg gggccccctc atgtgccagg 800
 tggacggcgc ctggctgctg gccggcatca tcagctgggg cgagggtgt 850
 gccgagcgca acaggcccgg ggtctacatc agcctctctg cgcaccgctc 900
 ctgggtggag aagatcgtgc aaggggtgca gctccgcggg cgcgctcagg 950
 ggggtggggc cctcagggca ccgagccagg gctctggggc cgcgcgcgc 1000
 tcctagggcg cagcgggacg cggggctcgg atctgaaagg cggccagatc 1050
 cacatctgga tctggatctg cggcgccctc gggcggtttc ccccgccgta 1100
 aataggctca tctacctta cctctggggg cccggacggc tgctgcggaa 1150

aggaaacccc ctccccgacc cgcccgacgg cctcaggccc cctccaagg 1200
catcaggccc cgcccaacgg cctcatgtcc ccgccccac gacttccggc 1250
cccgcccccg ggccccagcg cttttgtgta tataaatgtt aatgattttt 1300
ataggatatt gtaacctgc ccacatatct tatttattcc tccaatttca 1350
ataaattatt tattctccaa aaaaaaaaa 1378

<210> 263

<211> 317

<212> PRT

<213> Homo Sapien

<400> 263

| | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Val | Val | Ser | Gly | Ala | Pro | Pro | Ala | Leu | Gly | Gly | Gly | Cys | Leu | 1 | 5 | 10 | 15 |
| Gly | Thr | Phe | Thr | Ser | Leu | Leu | Leu | Ala | Ser | Thr | Ala | Ile | Leu | | 20 | 25 | 30 | |
| Asn | Ala | Ala | Arg | Ile | Pro | Val | Pro | Pro | Ala | Cys | Gly | Lys | Pro | Gln | 35 | 40 | 45 | |
| Gln | Leu | Asn | Arg | Val | Val | Gly | Gly | Glu | Asp | Ser | Thr | Asp | Ser | Glu | 50 | 55 | 60 | |
| Trp | Pro | Trp | Ile | Val | Ser | Ile | Gln | Lys | Asn | Gly | Thr | His | His | Cys | 65 | 70 | 75 | |
| Ala | Gly | Ser | Leu | Leu | Thr | Ser | Arg | Trp | Val | Ile | Thr | Ala | Ala | His | 80 | 85 | 90 | |
| Cys | Phe | Lys | Asp | Asn | Leu | Asn | Lys | Pro | Tyr | Leu | Phe | Ser | Val | Leu | 95 | 100 | 105 | |
| Leu | Gly | Ala | Trp | Gln | Leu | Gly | Asn | Pro | Gly | Ser | Arg | Ser | Gln | Lys | 110 | 115 | 120 | |
| Val | Gly | Val | Ala | Trp | Val | Glu | Pro | His | Pro | Val | Tyr | Ser | Trp | Lys | 125 | 130 | 135 | |
| Glu | Gly | Ala | Cys | Ala | Asp | Ile | Ala | Leu | Val | Arg | Leu | Glu | Arg | Ser | 140 | 145 | 150 | |
| Ile | Gln | Phe | Ser | Glu | Arg | Val | Leu | Pro | Ile | Cys | Leu | Pro | Asp | Ala | 155 | 160 | 165 | |
| Ser | Ile | His | Leu | Pro | Pro | Asn | Thr | His | Cys | Trp | Ile | Ser | Gly | Trp | 170 | 175 | 180 | |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Ser | Ile | Gln | Asp | Gly | Val | Pro | Leu | Pro | His | Pro | Gln | Thr | Leu |
| | | | | 185 | | | | | 190 | | | | | 195 |
| Gln | Lys | Leu | Lys | Val | Pro | Ile | Ile | Asp | Ser | Glu | Val | Cys | Ser | His |
| | | | | 200 | | | | | 205 | | | | | 210 |
| Leu | Tyr | Trp | Arg | Gly | Ala | Gly | Gln | Gly | Pro | Ile | Thr | Glu | Asp | Met |
| | | | | 215 | | | | | 220 | | | | | 225 |
| Leu | Cys | Ala | Gly | Tyr | Leu | Glu | Gly | Glu | Arg | Asp | Ala | Cys | Leu | Gly |
| | | | | 230 | | | | | 235 | | | | | 240 |
| Asp | Ser | Gly | Gly | Pro | Leu | Met | Cys | Gln | Val | Asp | Gly | Ala | Trp | Leu |
| | | | | 245 | | | | | 250 | | | | | 255 |
| Leu | Ala | Gly | Ile | Ile | Ser | Trp | Gly | Glu | Gly | Cys | Ala | Glu | Arg | Asn |
| | | | | 260 | | | | | 265 | | | | | 270 |
| Arg | Pro | Gly | Val | Tyr | Ile | Ser | Leu | Ser | Ala | His | Arg | Ser | Trp | Val |
| | | | | 275 | | | | | 280 | | | | | 285 |
| Glu | Lys | Ile | Val | Gln | Gly | Val | Gln | Leu | Arg | Gly | Arg | Ala | Gln | Gly |
| | | | | 290 | | | | | 295 | | | | | 300 |
| Gly | Gly | Ala | Leu | Arg | Ala | Pro | Ser | Gln | Gly | Ser | Gly | Ala | Ala | Ala |
| | | | | 305 | | | | | 310 | | | | | 315 |

Arg Ser

<210> 264

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 264

gtccgcaagg atgcctacat gttc 24

<210> 265

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 265

gcagaggtgt ctaaggttg 19

<210> 266

<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 266
agctctagac caatgccagc ttcc 24

<210> 267
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 267
gccaccaact cctgcaagaa cttctcagaa ctgcccctgg tcatg 45

<210> 268
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 268
ggggaattca ccctatgaca ttgcc 25

<210> 269
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 269
gaatgccctg caagcatcaa ctgg 24

<210> 270
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 270
gcacctgtca cctacactaa acacatccag cccatctgtc tccaggcctc 50

<210> 271
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 271
gcggaagggc agaatgggac tccaag 26

<210> 272
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 272
cagccctgcc acatgtgc 18

<210> 273
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 273
tactgggtgg tcagcaac 18

<210> 274
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 274
ggcgaagagc agggtagac cccg 24

<210> 275
<211> 45

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 275
gccctcatcc tctctggcaa atgcagttac agcccggagc ccgac 45

<210> 276
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 276
gggcagggat tccagggctc c 21

<210> 277
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 277
ggctatgaca gcaggttc 18

<210> 278
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 278
tgacaatgac cgaccagg 18

<210> 279
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 279
gcatcgatt gctggttagag caag 24

<210> 280
<211> 45
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 280

ttacagtgcc ccctggaaac ccacttggcc tgcataccgc ctccc 45

<210> 281

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 281

cgtctcgagc gctccatata gttcccttgc ccca 34

<210> 282

<211> 61

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 282

tggaggggga gcgggatgct tgtctgggag actccggggg cccctcatg 50

tgccaggtgg a 61

<210> 283

<211> 119

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 283

ccctcagacc ctgcagaagc tgaaggttcc tatcatcgac tcggaagtct 50

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atgctgtgtg ccggtact 119

<210> 284

<211> 1875

<212> DNA

<213> Homo Sapien

<400> 284

gacggctggc caccatgcac ggctcctgca gtttctgat gcttctgctg 50

ccgtactgc tactgctggt ggccaccaca ggccccgttg gagccctcac 100

[illegible]

ttctgaatgg gataccactc aaagggtgaa gaggtcagct gtcctcctgt 1450
 catcttcccc accctgtccc cagcccctaa acaagatact tcttggttaa 1500
 ggccctccgg aagggaaagg ctacggggca tgtgcctcat cacaccatcc 1550
 atcctggagg cacaaggcct ggctggctgc gagctcagga ggccgcctga 1600
 ggactgcaca ccggggccac acctctcctg cccctccctc ctgagtcctg 1650
 ggggtgggag gatttgaggg agctcactgc ctacctggcc tggggctgtc 1700
 tgccacacaca gcatgtgcgc tctccctgag tgcctgtgta gctggggatg 1750
 gggattccta ggggcagatg aaggacaagc cccactggag tggggttctt 1800
 tgagtggggg aggcagggac gagggaagga aagtaactcc tgactctcca 1850
 ataaaaacct gtccaacctg tgaaa 1875

<210> 285

<211> 463

<212> PRT

<213> Homo Sapien

<400> 285

| | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | His | Gly | Ser | Cys | Ser | Phe | Leu | Met | Leu | Leu | Leu | Pro | Leu | Leu | 1 | 5 | 10 | 15 |
| Leu | Leu | Leu | Val | Ala | Thr | Thr | Gly | Pro | Val | Gly | Ala | Leu | Thr | Asp | 20 | 25 | 30 | |
| Glu | Glu | Lys | Arg | Leu | Met | Val | Glu | Leu | His | Asn | Leu | Tyr | Arg | Ala | 35 | 40 | 45 | |
| Gln | Val | Ser | Pro | Thr | Ala | Ser | Asp | Met | Leu | His | Met | Arg | Trp | Asp | 50 | 55 | 60 | |
| Glu | Glu | Leu | Ala | Ala | Phe | Ala | Lys | Ala | Tyr | Ala | Arg | Gln | Cys | Val | 65 | 70 | 75 | |
| Trp | Gly | His | Asn | Lys | Glu | Arg | Gly | Arg | Arg | Gly | Glu | Asn | Leu | Phe | 80 | 85 | 90 | |
| Ala | Ile | Thr | Asp | Glu | Gly | Met | Asp | Val | Pro | Leu | Ala | Met | Glu | Glu | 95 | 100 | 105 | |
| Trp | His | His | Glu | Arg | Glu | His | Tyr | Asn | Leu | Ser | Ala | Ala | Thr | Cys | 110 | 115 | 120 | |
| Ser | Pro | Gly | Gln | Met | Cys | Gly | His | Tyr | Thr | Gln | Val | Val | Trp | Ala | 125 | 130 | 135 | |

| | | |
|-----------------|---------------------|-------------------------|
| Lys Thr Glu Arg | Ile Gly Cys Gly Ser | His Phe Cys Glu Lys Leu |
| 140 | 145 | 150 |
| Gln Gly Val Glu | Glu Thr Asn Ile Glu | Leu Leu Val Cys Asn Tyr |
| 155 | 160 | 165 |
| Glu Pro Pro Gly | Asn Val Lys Gly Lys | Arg Pro Tyr Gln Glu Gly |
| 170 | 175 | 180 |
| Thr Pro Cys Ser | Gln Cys Pro Ser Gly | Tyr His Cys Lys Asn Ser |
| 185 | 190 | 195 |
| Leu Cys Glu Pro | Ile Gly Ser Pro Glu | Asp Ala Gln Asp Leu Pro |
| 200 | 205 | 210 |
| Tyr Leu Val Thr | Glu Ala Pro Ser Phe | Arg Ala Thr Glu Ala Ser |
| 215 | 220 | 225 |
| Asp Ser Arg Lys | Met Gly Thr Pro Ser | Ser Leu Ala Thr Gly Ile |
| 230 | 235 | 240 |
| Pro Ala Phe Leu | Val Thr Glu Val Ser | Gly Ser Leu Ala Thr Lys |
| 245 | 250 | 255 |
| Ala Leu Pro Ala | Val Glu Thr Gln Ala | Pro Thr Ser Leu Ala Thr |
| 260 | 265 | 270 |
| Lys Asp Pro Pro | Ser Met Ala Thr Glu | Ala Pro Pro Cys Val Thr |
| 275 | 280 | 285 |
| Thr Glu Val Pro | Ser Ile Leu Ala Ala | His Ser Leu Pro Ser Leu |
| 290 | 295 | 300 |
| Asp Glu Glu Pro | Val Thr Phe Pro Lys | Ser Thr His Val Pro Ile |
| 305 | 310 | 315 |
| Pro Lys Ser Ala | Asp Lys Val Thr Asp | Lys Thr Lys Val Pro Ser |
| 320 | 325 | 330 |
| Arg Ser Pro Glu | Asn Ser Leu Asp Pro | Lys Met Ser Leu Thr Gly |
| 335 | 340 | 345 |
| Ala Arg Glu Leu | Leu Pro His Ala Gln | Glu Glu Ala Glu Ala Glu |
| 350 | 355 | 360 |
| Ala Glu Leu Pro | Pro Ser Ser Glu Val | Leu Ala Ser Val Phe Pro |
| 365 | 370 | 375 |
| Ala Gln Asp Lys | Pro Gly Glu Leu Gln | Ala Thr Leu Asp His Thr |
| 380 | 385 | 390 |
| Gly His Thr Ser | Ser Lys Ser Leu Pro | Asn Phe Pro Asn Thr Ser |
| 395 | 400 | 405 |

Ala Thr Ala Asn Ala Thr Gly Gly Arg Ala Leu Ala Leu Gln Ser
 410 415 420

Ser Leu Pro Gly Ala Glu Gly Pro Asp Lys Pro Ser Val Val Ser
 425 430 435

Gly Leu Asn Ser Gly Pro Gly His Val Trp Gly Pro Leu Leu Gly
 440 445 450

Leu Leu Leu Leu Pro Pro Leu Val Leu Ala Gly Ile Phe
 455 460

<210> 286

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 286

tcctgcagtt tcctgatgc 19

<210> 287

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 287

ctcatattgc acaccagtaa ttcg 24

<210> 288

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 288

atgaggagaa acgtttgatg gtggagctgc acaacctcta ccggg 45

<210> 289

<211> 3662

<212> DNA

<213> Homo Sapien

<400> 289

gtaactgaag tcaggctttt catttgggaa gccccctcaa cagaattcgg 50

[illegible]

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 gccagcagca gtgattcccc aatgactttt gotttgaaaa aagacaatga 1500
 actactgcat gatgctgaaa tggaaaatta tgcacacctc cgggcccaag 1550
 gtggcgaggt gatggagtat accaccatcc ttgggtgctg cgaggtggaa 1600
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 ccgaggatga cgtgttcttt atcgtggatg tgaagataga ggacattggg 1900
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 aaccgagagg cacttttttg cagcaggcaa tcagcttctg attattgtgg 2150
 actcagatgt cagtgatgct gggaaataca catgtgagat gtctaacc 2200
 cttggcactg agagaggaaa cgtgcgcctc agtgtgatcc cactccaac 2250
 ctgcgactcc cctcagatga cagccccatc gttagacgat gacggatggg 2300
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 ttgcagcatt accaacacag atgagaccaa cttgccagca gatattccta 2450
 gttatttgtc atctcagga acgttagctg acaggcagga tgggtacgtg 2500
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 actacaggac tccaaatttt cagtcttatg acttggacac atagactgaa 3250
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<210> 290

<211> 1059

<212> PRT

<213> Homo Sapien

<400> 290

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Asp | Val | Leu | Leu | Leu | Phe | Ser | Leu | Cys | Leu | Leu | Phe | His |
| 1 | | | | 5 | | | | | 10 | | | | 15 | |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Ser | Arg | Pro | Asp | Leu | Ser | His | Asn | Arg | Leu | Ser | Phe | Ile | Lys |
| | | | | 20 | | | | 25 | | | | | 30 | |

| | | | |
|---|-----|-----|-----|
| Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu | 35 | 40 | 45 |
| Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser | 50 | 55 | 60 |
| Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu | 65 | 70 | 75 |
| Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu | 80 | 85 | 90 |
| Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro | 95 | 100 | 105 |
| Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr | 110 | 115 | 120 |
| Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu | 125 | 130 | 135 |
| Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys | 140 | 145 | 150 |
| Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn | 155 | 160 | 165 |
| Lys Ile Lys Asn Val Asp Gly Leu Thr Phe Gln Gly Leu Gly Ala | 170 | 175 | 180 |
| Leu Lys Ser Leu Lys Met Gln Arg Asn Gly Val Thr Lys Leu Met | 185 | 190 | 195 |
| Asp Gly Ala Phe Trp Gly Leu Ser Asn Met Glu Ile Leu Gln Leu | 200 | 205 | 210 |
| Asp His Asn Asn Leu Thr Glu Ile Thr Lys Gly Trp Leu Tyr Gly | 215 | 220 | 225 |
| Leu Leu Met Leu Gln Glu Leu His Leu Ser Gln Asn Ala Ile Asn | 230 | 235 | 240 |
| Arg Ile Ser Pro Asp Ala Trp Glu Phe Cys Gln Lys Leu Ser Glu | 245 | 250 | 255 |
| Leu Asp Leu Thr Phe Asn His Leu Ser Arg Leu Asp Asp Ser Ser | 260 | 265 | 270 |
| Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn | 275 | 280 | 285 |
| Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser | | | |

| | | |
|---|-----|-----|
| 290 | 295 | 300 |
| Leu Lys Thr Leu Asp Leu Lys Asn Asn Glu Ile Ser Trp Thr Ile | | |
| 305 | 310 | 315 |
| Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg | | |
| 320 | 325 | 330 |
| Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala | | |
| 335 | 340 | 345 |
| Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn | | |
| 350 | 355 | 360 |
| Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys | | |
| 365 | 370 | 375 |
| Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys | | |
| 380 | 385 | 390 |
| Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln | | |
| 395 | 400 | 405 |
| Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly | | |
| 410 | 415 | 420 |
| Arg Ser Ile Phe Ala Val Ser Pro Asp Gly Phe Val Cys Asp Asp | | |
| 425 | 430 | 435 |
| Phe Pro Lys Pro Gln Ile Thr Val Gln Pro Glu Thr Gln Ser Ala | | |
| 440 | 445 | 450 |
| Ile Lys Gly Ser Asn Leu Ser Phe Ile Cys Ser Ala Ala Ser Ser | | |
| 455 | 460 | 465 |
| Ser Asp Ser Pro Met Thr Phe Ala Trp Lys Lys Asp Asn Glu Leu | | |
| 470 | 475 | 480 |
| Leu His Asp Ala Glu Met Glu Asn Tyr Ala His Leu Arg Ala Gln | | |
| 485 | 490 | 495 |
| Gly Gly Glu Val Met Glu Tyr Thr Thr Ile Leu Arg Leu Arg Glu | | |
| 500 | 505 | 510 |
| Val Glu Phe Ala Ser Glu Gly Lys Tyr Gln Cys Val Ile Ser Asn | | |
| 515 | 520 | 525 |
| His Phe Gly Ser Ser Tyr Ser Val Lys Ala Lys Leu Thr Val Asn | | |
| 530 | 535 | 540 |
| Met Leu Pro Ser Phe Thr Lys Thr Pro Met Asp Leu Thr Ile Arg | | |
| 545 | 550 | 555 |

| | | | |
|-----------------|---------------------|---------------------|-----|
| Ala Gly Ala Met | Ala Arg Leu Glu Cys | Ala Ala Val Gly His | Pro |
| 560 | 565 | | 570 |
| Ala Pro Gln Ile | Ala Trp Gln Lys Asp | Gly Gly Thr Asp Phe | Pro |
| 575 | 580 | | 585 |
| Ala Ala Arg Glu | Arg Arg Met His Val | Met Pro Glu Asp Asp | Val |
| 590 | 595 | | 600 |
| Phe Phe Ile Val | Asp Val Lys Ile Glu | Asp Ile Gly Val Tyr | Ser |
| 605 | 610 | | 615 |
| Cys Thr Ala Gln | Asn Ser Ala Gly Ser | Ile Ser Ala Asn Ala | Thr |
| 620 | 625 | | 630 |
| Leu Thr Val Leu | Glu Thr Pro Ser Phe | Leu Arg Pro Leu Leu | Asp |
| 635 | 640 | | 645 |
| Arg Thr Val Thr | Lys Gly Glu Thr Ala | Val Leu Gln Cys Ile | Ala |
| 650 | 655 | | 660 |
| Gly Gly Ser Pro | Pro Pro Lys Leu Asn | Trp Thr Lys Asp Asp | Ser |
| 665 | 670 | | 675 |
| Pro Leu Val Val | Thr Glu Arg His Phe | Phe Ala Ala Gly Asn | Gln |
| 680 | 685 | | 690 |
| Leu Leu Ile Ile | Val Asp Ser Asp Val | Ser Asp Ala Gly Lys | Tyr |
| 695 | 700 | | 705 |
| Thr Cys Glu Met | Ser Asn Thr Leu Gly | Thr Glu Arg Gly Asn | Val |
| 710 | 715 | | 720 |
| Arg Leu Ser Val | Ile Pro Thr Pro Thr | Cys Asp Ser Pro Gln | Met |
| 725 | 730 | | 735 |
| Thr Ala Pro Ser | Leu Asp Asp Asp Gly | Trp Ala Thr Val Gly | Val |
| 740 | 745 | | 750 |
| Val Ile Ile Ala | Val Val Cys Cys Val | Val Gly Thr Ser Leu | Val |
| 755 | 760 | | 765 |
| Trp Val Val Ile | Ile Tyr His Thr Arg | Arg Arg Asn Glu Asp | Cys |
| 770 | 775 | | 780 |
| Ser Ile Thr Asn | Thr Asp Glu Thr Asn | Leu Pro Ala Asp Ile | Pro |
| 785 | 790 | | 795 |
| Ser Tyr Leu Ser | Ser Gln Gly Thr Leu | Ala Asp Arg Gln Asp | Gly |
| 800 | 805 | | 810 |

Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser
 815 820 825
 Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr
 830 835 840
 Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr
 845 850 855
 Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr
 860 865 870
 Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His
 875 880 885
 Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr
 890 895 900
 Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His
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 Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp
 920 925 930
 Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn
 935 940 945
 Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu
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 965 970 975
 Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu
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 Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg
 995 1000 1005
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 Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn
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<210> 291

<211> 2906

<212> DNA

<213> Homo Sapien

<400> 291

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<211> 640

<212> PRT

<213> Homo Sapien

<400> 292

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Asn | Lys | Met | Thr | Leu | His | Pro | Gln | Gln | Ile | Met | Ile | Gly |
| 1 | | | | 5 | | | | | 10 | | | | | 15 |
| Pro | Arg | Phe | Asn | Arg | Ala | Leu | Phe | Asp | Pro | Leu | Leu | Val | Val | Leu |
| | | | | 20 | | | | | 25 | | | | | 30 |
| Leu | Ala | Leu | Gln | Leu | Leu | Val | Val | Ala | Gly | Leu | Val | Arg | Ala | Gln |
| | | | | 35 | | | | | 40 | | | | | 45 |
| Thr | Cys | Pro | Ser | Val | Cys | Ser | Cys | Ser | Asn | Gln | Phe | Ser | Lys | Val |
| | | | | 50 | | | | | 55 | | | | | 60 |
| Ile | Cys | Val | Arg | Lys | Asn | Leu | Arg | Glu | Val | Pro | Asp | Gly | Ile | Ser |
| | | | | 65 | | | | | 70 | | | | | 75 |
| Thr | Asn | Thr | Arg | Leu | Leu | Asn | Leu | His | Glu | Asn | Gln | Ile | Gln | Ile |
| | | | | 80 | | | | | 85 | | | | | 90 |
| Ile | Lys | Val | Asn | Ser | Phe | Lys | His | Leu | Arg | His | Leu | Glu | Ile | Leu |
| | | | | 95 | | | | | 100 | | | | | 105 |
| Gln | Leu | Ser | Arg | Asn | His | Ile | Arg | Thr | Ile | Glu | Ile | Gly | Ala | Phe |
| | | | | 110 | | | | | 115 | | | | | 120 |
| Asn | Gly | Leu | Ala | Asn | Leu | Asn | Thr | Leu | Glu | Leu | Phe | Asp | Asn | Arg |
| | | | | 125 | | | | | 130 | | | | | 135 |
| Leu | Thr | Thr | Ile | Pro | Asn | Gly | Ala | Phe | Val | Tyr | Leu | Ser | Lys | Leu |
| | | | | 140 | | | | | 145 | | | | | 150 |
| Lys | Glu | Leu | Trp | Leu | Arg | Asn | Asn | Pro | Ile | Glu | Ser | Ile | Pro | Ser |

| | | | | | |
|---|-----|--|-----|--|-----|
| | 155 | | 160 | | 165 |
| Tyr Ala Phe Asn Arg Ile Pro Ser Leu Arg Arg Leu Asp Leu Gly | 170 | | 175 | | 180 |
| Glu Leu Lys Arg Leu Ser Tyr Ile Ser Glu Gly Ala Phe Glu Gly | 185 | | 190 | | 195 |
| Leu Ser Asn Leu Arg Tyr Leu Asn Leu Ala Met Cys Asn Leu Arg | 200 | | 205 | | 210 |
| Glu Ile Pro Asn Leu Thr Pro Leu Ile Lys Leu Asp Glu Leu Asp | 215 | | 220 | | 225 |
| Leu Ser Gly Asn His Leu Ser Ala Ile Arg Pro Gly Ser Phe Gln | 230 | | 235 | | 240 |
| Gly Leu Met His Leu Gln Lys Leu Trp Met Ile Gln Ser Gln Ile | 245 | | 250 | | 255 |
| Gln Val Ile Glu Arg Asn Ala Phe Asp Asn Leu Gln Ser Leu Val | 260 | | 265 | | 270 |
| Glu Ile Asn Leu Ala His Asn Asn Leu Thr Leu Leu Pro His Asp | 275 | | 280 | | 285 |
| Leu Phe Thr Pro Leu His His Leu Glu Arg Ile His Leu His His | 290 | | 295 | | 300 |
| Asn Pro Trp Asn Cys Asn Cys Asp Ile Leu Trp Leu Ser Trp Trp | 305 | | 310 | | 315 |
| Ile Lys Asp Met Ala Pro Ser Asn Thr Ala Cys Cys Ala Arg Cys | 320 | | 325 | | 330 |
| Asn Thr Pro Pro Asn Leu Lys Gly Arg Tyr Ile Gly Glu Leu Asp | 335 | | 340 | | 345 |
| Gln Asn Tyr Phe Thr Cys Tyr Ala Pro Val Ile Val Glu Pro Pro | 350 | | 355 | | 360 |
| Ala Asp Leu Asn Val Thr Glu Gly Met Ala Ala Glu Leu Lys Cys | 365 | | 370 | | 375 |
| Arg Ala Ser Thr Ser Leu Thr Ser Val Ser Trp Ile Thr Pro Asn | 380 | | 385 | | 390 |
| Gly Thr Val Met Thr His Gly Ala Tyr Lys Val Arg Ile Ala Val | 395 | | 400 | | 405 |
| Leu Ser Asp Gly Thr Leu Asn Phe Thr Asn Val Thr Val Gln Asp | 410 | | 415 | | 420 |

Thr Gly Met Tyr Thr Cys Met Val Ser Asn Ser Val Gly Asn Thr
 425 430 435
 Thr Ala Ser Ala Thr Leu Asn Val Thr Ala Ala Thr Thr Thr Pro
 440 445 450
 Phe Ser Tyr Phe Ser Thr Val Thr Val Glu Thr Met Glu Pro Ser
 455 460 465
 Gln Asp Glu Ala Arg Thr Thr Asp Asn Asn Val Gly Pro Thr Pro
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 575 580 585
 Pro Met Pro Ala Ile Glu His Glu His Leu Asn His Tyr Asn Ser
 590 595 600
 Tyr Lys Ser Pro Phe Asn His Thr Thr Thr Val Asn Thr Ile Asn
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<211> 4053

<212> DNA

<213> Homo Sapien

<400> 293

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<213> Homo Sapien

<400> 294

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Pro Cys Pro Thr Thr Cys Arg Cys Leu Gly Asp Leu Leu Asp Cys
50 55 60

Ser Arg Lys Arg Leu Ala Arg Leu Pro Glu Pro Leu Pro Ser Trp
65 70 75

Val Ala Arg Leu Asp Leu Ser His Asn Arg Leu Ser Phe Ile Lys
80 85 90

Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu
95 100 105

Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser
110 115 120

Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu
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Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu
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Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro
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Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr
170 175 180

Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu
185 190 195

Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys
200 205 210

Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn

| | | |
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| Lys Ile Lys Asn Val Asp Gly Leu Thr | Phe Gln Gly Leu Gly | Ala |
| 230 | 235 | 240 |
| Leu Lys Ser Leu Lys Met Gln Arg Asn | Gly Val Thr Lys Leu | Met |
| 245 | 250 | 255 |
| Asp Gly Ala Phe Trp Gly Leu Ser Asn | Met Glu Ile Leu Gln | Leu |
| 260 | 265 | 270 |
| Asp His Asn Asn Leu Thr Glu Ile Thr | Lys Gly Trp Leu Tyr | Gly |
| 275 | 280 | 285 |
| Leu Leu Met Leu Gln Glu Leu His Leu | Ser Gln Asn Ala Ile | Asn |
| 290 | 295 | 300 |
| Arg Ile Ser Pro Asp Ala Trp Glu Phe | Cys Gln Lys Leu Ser | Glu |
| 305 | 310 | 315 |
| Leu Asp Leu Thr Phe Asn His Leu Ser | Arg Leu Asp Asp Ser | Ser |
| 320 | 325 | 330 |
| Phe Leu Gly Leu Ser Leu Leu Asn Thr | Leu His Ile Gly Asn | Asn |
| 335 | 340 | 345 |
| Arg Val Ser Tyr Ile Ala Asp Cys Ala | Phe Arg Gly Leu Ser | Ser |
| 350 | 355 | 360 |
| Leu Lys Thr Leu Asp Leu Lys Asn Asn | Glu Ile Ser Trp Thr | Ile |
| 365 | 370 | 375 |
| Glu Asp Met Asn Gly Ala Phe Ser Gly | Leu Asp Lys Leu Arg | Arg |
| 380 | 385 | 390 |
| Leu Ile Leu Gln Gly Asn Arg Ile Arg | Ser Ile Thr Lys Lys | Ala |
| 395 | 400 | 405 |
| Phe Thr Gly Leu Asp Ala Leu Glu His | Leu Asp Leu Ser Asp | Asn |
| 410 | 415 | 420 |
| Ala Ile Met Ser Leu Gln Gly Asn Ala | Phe Ser Gln Met Lys | Lys |
| 425 | 430 | 435 |
| Leu Gln Gln Leu His Leu Asn Thr Ser | Ser Leu Leu Cys Asp | Cys |
| 440 | 445 | 450 |
| Gln Leu Lys Trp Leu Pro Gln Trp Val | Ala Glu Asn Asn Phe | Gln |
| 455 | 460 | 465 |
| Ser Phe Val Asn Ala Ser Cys Ala His | Pro Gln Leu Leu Lys | Gly |
| 470 | 475 | 480 |

| | | | |
|---|-----|-----|-----|
| Arg Ser Ile Phe Ala Val Ser Pro Asp Gly Phe Val Cys Asp Asp | 485 | 490 | 495 |
| Phe Pro Lys Pro Gln Ile Thr Val Gln Pro Glu Thr Gln Ser Ala | 500 | 505 | 510 |
| Ile Lys Gly Ser Asn Leu Ser Phe Ile Cys Ser Ala Ala Ser Ser | 515 | 520 | 525 |
| Ser Asp Ser Pro Met Thr Phe Ala Trp Lys Lys Asp Asn Glu Leu | 530 | 535 | 540 |
| Leu His Asp Ala Glu Met Glu Asn Tyr Ala His Leu Arg Ala Gln | 545 | 550 | 555 |
| Gly Gly Glu Val Met Glu Tyr Thr Thr Ile Leu Arg Leu Arg Glu | 560 | 565 | 570 |
| Val Glu Phe Ala Ser Glu Gly Lys Tyr Gln Cys Val Ile Ser Asn | 575 | 580 | 585 |
| His Phe Gly Ser Ser Tyr Ser Val Lys Ala Lys Leu Thr Val Asn | 590 | 595 | 600 |
| Met Leu Pro Ser Phe Thr Lys Thr Pro Met Asp Leu Thr Ile Arg | 605 | 610 | 615 |
| Ala Gly Ala Met Ala Arg Leu Glu Cys Ala Ala Val Gly His Pro | 620 | 625 | 630 |
| Ala Pro Gln Ile Ala Trp Gln Lys Asp Gly Gly Thr Asp Phe Pro | 635 | 640 | 645 |
| Ala Ala Arg Glu Arg Arg Met His Val Met Pro Glu Asp Asp Val | 650 | 655 | 660 |
| Phe Phe Ile Val Asp Val Lys Ile Glu Asp Ile Gly Val Tyr Ser | 665 | 670 | 675 |
| Cys Thr Ala Gln Asn Ser Ala Gly Ser Ile Ser Ala Asn Ala Thr | 680 | 685 | 690 |
| Leu Thr Val Leu Glu Thr Pro Ser Phe Leu Arg Pro Leu Leu Asp | 695 | 700 | 705 |
| Arg Thr Val Thr Lys Gly Glu Thr Ala Val Leu Gln Cys Ile Ala | 710 | 715 | 720 |
| Gly Gly Ser Pro Pro Pro Lys Leu Asn Trp Thr Lys Asp Asp Ser | 725 | 730 | 735 |
| Pro Leu Val Val Thr Glu Arg His Phe Phe Ala Ala Gly Asn Gln | 740 | 745 | 750 |

Leu Leu Ile Ile Val Asp Ser Asp Val Ser Asp Ala Gly Lys Tyr
 755 760 765
 Thr Cys Glu Met Ser Asn Thr Leu Gly Thr Glu Arg Gly Asn Val
 770 775 780
 Arg Leu Ser Val Ile Pro Thr Pro Thr Cys Asp Ser Pro Gln Met
 785 790 795
 Thr Ala Pro Ser Leu Asp Asp Asp Gly Trp Ala Thr Val Gly Val
 800 805 810
 Val Ile Ile Ala Val Val Cys Cys Val Val Gly Thr Ser Leu Val
 815 820 825
 Trp Val Val Ile Ile Tyr His Thr Arg Arg Arg Asn Glu Asp Cys
 830 835 840
 Ser Ile Thr Asn Thr Asp Glu Thr Asn Leu Pro Ala Asp Ile Pro
 845 850 855
 Ser Tyr Leu Ser Ser Gln Gly Thr Leu Ala Asp Arg Gln Asp Gly
 860 865 870
 Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser
 875 880 885
 Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr
 890 895 900
 Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr
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 Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr
 920 925 930
 Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His
 935 940 945
 Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr
 950 955 960
 Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His
 965 970 975
 Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp
 980 985 990
 Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn
 995 1000 1005
 Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu

| 1010 | 1015 | 1020 |
|---|------|------|
| Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn | | |
| 1025 | 1030 | 1035 |
| Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu | | |
| 1040 | 1045 | 1050 |
| Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg | | |
| 1055 | 1060 | 1065 |
| Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly | | |
| 1070 | 1075 | 1080 |
| Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn | | |
| 1085 | 1090 | 1095 |
| His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro | | |
| 1100 | 1105 | 1110 |
| Asn Phe Gln Ser Tyr Asp Leu Asp Thr | | |
| 1115 | | |
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| <220> | | |
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| ggaaccgaat ctcagcta 18 | | |
| <210> 296 | | |
| <211> 19 | | |
| <212> DNA | | |
| <213> Artificial Sequence | | |
| <220> | | |
| <223> Synthetic Oligonucleotide Probe | | |
| <400> 296 | | |
| cctaaactga actggacca 19 | | |
| <210> 297 | | |
| <211> 19 | | |
| <212> DNA | | |
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ggctggagac actgaacct 19

<210> 298
<211> 24
<212> DNA
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<400> 300
gggtcttggt gaatgagg 18

<210> 301
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<400> 301
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<210> 302
<211> 50
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<220>

<223> Synthetic Oligonucleotide Probe

<400> 302

gcggccactg ttggaccgaa ctgtaaccaa gggagaaaca gccgtcctac 50

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<211> 28

<212> DNA

<213> Artificial Sequence

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<400> 303

gcctttgaca accttcagtc actagtgg 28

<210> 304

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 304

ccccatgtgt ccatgactgt tccc 24

<210> 305

<211> 45

<212> DNA

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 305

tactgcctca tgacctcttc actcccttgc atcatcttag agcgg 45

<210> 306

<211> 24

<212> DNA

<213> Artificial Sequence

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<400> 306

actccaagga aatcggatcc gttc 24

<210> 307

<211> 24

<212> DNA
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<220>
 <223> Synthetic oligonucleotide probe

<400> 307
 ttagcagctg aggatgggca caac 24

<210> 308
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<400> 308
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<210> 309
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<400> 309
 gccttcaactg gtttggatgc attggagcat ctagacctga gtgacaacgc 50

<210> 310
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 <212> DNA
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<400> 310

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 ctgctccacg aggcgccact ggtgtgaacc gggagagccc ctgggtggtc 200
 ccgtcccccta tccctccttt atatagaaac cttccacact ggaaggcag 250
 cggcgaggca ggagggtca tggtagcaa ggaggccggc tgatctgcag 300
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 gaggaggcag aacagcctgc ctggttccat cagccctggc gccagggcg 400

| | | | | | |
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| tgctcctgct | gctgctgccg | ccacagctgc | acctgggacc | tgtgcttgcc | 500 |
| gtgagggccc | caggatttgg | ccgaagtggc | ggccacagcc | tgagccccga | 550 |
| agagaacgaa | tttgcgagg | aggagccggt | gctggtactg | agccctgagg | 600 |
| agcccgggcc | tggcccagcc | gcggtcagct | gcccccgaga | ctgtgcctgt | 650 |
| tcccaggagg | gcgtcgtgga | ctgtggcggt | attgacctgc | gtgagttccc | 700 |
| gggggacctg | cctgagcaca | ccaaccacct | atctctgcag | aacaaccagc | 750 |
| tggaaaagat | ctaccctgag | gagctctccc | ggctgcaccg | gctggagaca | 800 |
| ctgaacctgc | aaaacaaccg | cctgacttcc | cgagggctcc | cagagaaggc | 850 |
| gtttgagcat | ctgaccaacc | tcaattacct | gtacttggcc | aataacaagc | 900 |
| tgaccttggc | accccgcttc | ctgccaaacg | ccctgatcag | tgtggacttt | 950 |
| gctgccaact | atctcaccaa | gatctatggg | ctcacctttg | gccagaagcc | 1000 |
| aaacttgagg | tctgtgtacc | tgcacaacaa | caagctggca | gacgccgggc | 1050 |
| tgccggacaa | catgttcaac | ggctccagca | acgtcgaggt | cctcatcctg | 1100 |
| tccagcaact | tcttgccca | cgtgcccagg | cacctgccgc | ctgccctgta | 1150 |
| caagctgcac | ctcaagaaca | acaagctgga | gaagatcccc | ccgggggcct | 1200 |
| tcagcgagct | gagcagcctg | cgcgagctat | acctgcagaa | caactacctg | 1250 |
| actgacgagg | gcctggacaa | cgagaccttc | tggaagctct | ccagcctgga | 1300 |
| gtacctggat | ctgtccagca | acaacctgtc | tggggtccca | gctgggctgc | 1350 |
| cgcgcagcct | ggtgctgctg | cacttgagga | agaacgccat | ccggagcgtg | 1400 |
| gacgcgaatg | tgctgacccc | catccgcagc | ctggagtacc | tgctgctgca | 1450 |
| cagcaaccag | ctgcgggagc | agggcatcca | cccactggcc | ttccagggcc | 1500 |
| tcaagcggtt | gcacacggtg | cacctgtaca | acaacgcgct | ggagcgcgtg | 1550 |
| cccagtggcc | tgctcgccg | cgtgcgacc | ctcatgatcc | tgcacaacca | 1600 |
| gatcacaggc | attggccgcg | aagactttgc | caccacctac | ttcctggagg | 1650 |
| agctcaacct | cagctacaac | cgcatacca | gccacaggt | gcaccgcgac | 1700 |

gccttccgca agctgcgctt gctgcgctcg ctggacctgt cgggcaaccg 1750
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<220>
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<400> 311
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<210> 312
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 312
 gcggccacgg tccttggaat tg 22

<210> 313
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 313
 tggaggagct caacctcagc tacaaccgca tcaccagccc acagg 45

<210> 314
 <211> 3003
 <212> DNA
 <213> Homo Sapien

<400> 314
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 cgccgctgtc ctccgggagc ggcagcagta gcccggggcg cgagggtgg 100

[illegible]

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 gaccagcag gtggacaata tctgacagtg tcggcagcca aagccccagg 1500
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 gggacctgtg cctgtcattc aggcacaagg tgacgggggt gcactctggc 1600
 aactccagg tgtttgtgag aaaacacggt gccacaggag cagccctgtg 1650
 gggaagaaat ggtggccatg gctggaggca aacacagatc accttgcgag 1700
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 gcacagagag ggtggcgacc agctgttctc catatgcact aagaatagaa 1900
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 aat 3003

<210> 315

<211> 509

<212> PRT

<213> Homo Sapien

<400> 315

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| Met | Asp | Phe | Leu | Leu | Ala | Leu | Val | Leu | Val | Ser | Ser | Leu | Tyr | Leu | 1 | 5 | 10 | 15 |
| Gln | Ala | Ala | Ala | Glu | Phe | Asp | Gly | Arg | Trp | Pro | Arg | Gln | Ile | Val | 20 | 25 | 30 | |
| Ser | Ser | Ile | Gly | Leu | Cys | Arg | Tyr | Gly | Gly | Arg | Ile | Asp | Cys | Cys | 35 | 40 | 45 | |
| Trp | Gly | Trp | Ala | Arg | Gln | Ser | Trp | Gly | Gln | Cys | Gln | Pro | Val | Cys | 50 | 55 | 60 | |
| Gln | Pro | Arg | Cys | Lys | His | Gly | Glu | Cys | Ile | Gly | Pro | Asn | Lys | Cys | 65 | 70 | 75 | |
| Lys | Cys | His | Pro | Gly | Tyr | Ala | Gly | Lys | Thr | Cys | Asn | Gln | Asp | Leu | 80 | 85 | 90 | |
| Asn | Glu | Cys | Gly | Leu | Lys | Pro | Arg | Pro | Cys | Lys | His | Arg | Cys | Met | 95 | 100 | 105 | |
| Asn | Thr | Tyr | Gly | Ser | Tyr | Lys | Cys | Tyr | Cys | Leu | Asn | Gly | Tyr | Met | 110 | 115 | 120 | |
| Leu | Met | Pro | Asp | Gly | Ser | Cys | Ser | Ser | Ala | Leu | Thr | Cys | Ser | Met | 125 | 130 | 135 | |
| Ala | Asn | Cys | Gln | Tyr | Gly | Cys | Asp | Val | Val | Lys | Gly | Gln | Ile | Arg | 140 | 145 | 150 | |
| Cys | Gln | Cys | Pro | Ser | Pro | Gly | Leu | His | Leu | Ala | Pro | Asp | Gly | Arg | 155 | 160 | 165 | |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Cys | Val | Asp | Val | Asp | Glu | Cys | Ala | Thr | Gly | Arg | Ala | Ser | Cys |
| | | | | 170 | | | | | 175 | | | | | 180 |
| Pro | Arg | Phe | Arg | Gln | Cys | Val | Asn | Thr | Phe | Gly | Ser | Tyr | Ile | Cys |
| | | | | 185 | | | | | 190 | | | | | 195 |
| Lys | Cys | His | Lys | Gly | Phe | Asp | Leu | Met | Tyr | Ile | Gly | Gly | Lys | Tyr |
| | | | | 200 | | | | | 205 | | | | | 210 |
| Gln | Cys | His | Asp | Ile | Asp | Glu | Cys | Ser | Leu | Gly | Gln | Tyr | Gln | Cys |
| | | | | 215 | | | | | 220 | | | | | 225 |
| Ser | Ser | Phe | Ala | Arg | Cys | Tyr | Asn | Val | Arg | Gly | Ser | Tyr | Lys | Cys |
| | | | | 230 | | | | | 235 | | | | | 240 |
| Lys | Cys | Lys | Glu | Gly | Tyr | Gln | Gly | Asp | Gly | Leu | Thr | Cys | Val | Tyr |
| | | | | 245 | | | | | 250 | | | | | 255 |
| Ile | Pro | Lys | Val | Met | Ile | Glu | Pro | Ser | Gly | Pro | Ile | His | Val | Pro |
| | | | | 260 | | | | | 265 | | | | | 270 |
| Lys | Gly | Asn | Gly | Thr | Ile | Leu | Lys | Gly | Asp | Thr | Gly | Asn | Asn | Asn |
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| Trp | Ile | Pro | Asp | Val | Gly | Ser | Thr | Trp | Trp | Pro | Pro | Lys | Thr | Pro |
| | | | | 290 | | | | | 295 | | | | | 300 |
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| | | | | 335 | | | | | 340 | | | | | 345 |
| Thr | Pro | Glu | Arg | Pro | Thr | Thr | Gly | Leu | Thr | Thr | Ile | Ala | Pro | Ala |
| | | | | 350 | | | | | 355 | | | | | 360 |
| Ala | Ser | Thr | Pro | Pro | Gly | Gly | Ile | Thr | Val | Asp | Asn | Arg | Val | Gln |
| | | | | 365 | | | | | 370 | | | | | 375 |
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| | | | | 380 | | | | | 385 | | | | | 390 |
| His | Ser | Cys | Asn | Phe | Asp | His | Gly | Leu | Cys | Gly | Trp | Ile | Arg | Glu |
| | | | | 395 | | | | | 400 | | | | | 405 |
| Lys | Asp | Asn | Asp | Leu | His | Trp | Glu | Pro | Ile | Arg | Asp | Pro | Ala | Gly |
| | | | | 410 | | | | | 415 | | | | | 420 |
| Gly | Gln | Tyr | Leu | Thr | Val | Ser | Ala | Ala | Lys | Ala | Pro | Gly | Gly | Lys |

| | | |
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| Ala Ala Arg Leu Val Leu Pro Leu Gly Arg Leu Met His Ser Gly | | |
| 440 | 445 | 450 |
| Asp Leu Cys Leu Ser Phe Arg His Lys Val Thr Gly Leu His Ser | | |
| 455 | 460 | 465 |
| Gly Thr Leu Gln Val Phe Val Arg Lys His Gly Ala His Gly Ala | | |
| 470 | 475 | 480 |
| Ala Leu Trp Gly Arg Asn Gly Gly His Gly Trp Arg Gln Thr Gln | | |
| 485 | 490 | 495 |
| Ile Thr Leu Arg Gly Ala Asp Ile Lys Ser Glu Ser Gln Arg | | |
| 500 | 505 | |

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<220>
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<210> 317
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<220>
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<400> 317
 ttgcacttgt aggacccacg tacg 24

<210> 318
 <211> 50
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<220>
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<400> 318
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<210> 319
 <211> 2110
 <212> DNA

<213> Homo Sapien

<400> 319

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<210> 320

<211> 450

<212> PRT

<213> Homo Sapien

<400> 320

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| Met | Trp | Leu | Lys | Val | Phe | Thr | Thr | Phe | Leu | Ser | Phe | Ala | Thr | Gly |
| 1 | | | | 5 | | | | | 10 | | | | | 15 |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Cys | Ser | Gly | Leu | Lys | Val | Thr | Val | Pro | Ser | His | Thr | Val | His |
| | | | | 20 | | | | | 25 | | | | | 30 |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Val | Arg | Gly | Gln | Ala | Leu | Tyr | Leu | Pro | Val | His | Tyr | Gly | Phe |
| | | | | 35 | | | | | 40 | | | | | 45 |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Thr | Pro | Ala | Ser | Asp | Ile | Gln | Ile | Ile | Trp | Leu | Phe | Glu | Arg |
| | | | | 50 | | | | | 55 | | | | | 60 |

Pro His Thr Met Pro Lys Tyr Leu Leu Gly Ser Val Asn Lys Ser
 65 70 75
 Val Val Pro Asp Leu Glu Tyr Gln His Lys Phe Thr Met Met Pro
 80 85 90
 Pro Asn Ala Ser Leu Leu Ile Asn Pro Leu Gln Phe Pro Asp Glu
 95 100 105
 Gly Asn Tyr Ile Val Lys Val Asn Ile Gln Gly Asn Gly Thr Leu
 110 115 120
 Ser Ala Ser Gln Lys Ile Gln Val Thr Val Asp Asp Pro Val Thr
 125 130 135
 Lys Pro Val Val Gln Ile His Pro Pro Ser Gly Ala Val Glu Tyr
 140 145 150
 Val Gly Asn Met Thr Leu Thr Cys His Val Glu Gly Gly Thr Arg
 155 160 165
 Leu Ala Tyr Gln Trp Leu Lys Asn Gly Arg Pro Val His Thr Ser
 170 175 180
 Ser Thr Tyr Ser Phe Ser Pro Gln Asn Asn Thr Leu His Ile Ala
 185 190 195
 Pro Val Thr Lys Glu Asp Ile Gly Asn Tyr Ser Cys Leu Val Arg
 200 205 210
 Asn Pro Val Ser Glu Met Glu Ser Asp Ile Ile Met Pro Ile Ile
 215 220 225
 Tyr Tyr Gly Pro Tyr Gly Leu Gln Val Asn Ser Asp Lys Gly Leu
 230 235 240
 Lys Val Gly Glu Val Phe Thr Val Asp Leu Gly Glu Ala Ile Leu
 245 250 255
 Phe Asp Cys Ser Ala Asp Ser His Pro Pro Asn Thr Tyr Ser Trp
 260 265 270
 Ile Arg Arg Thr Asp Asn Thr Thr Tyr Ile Ile Lys His Gly Pro
 275 280 285
 Arg Leu Glu Val Ala Ser Glu Lys Val Ala Gln Lys Thr Met Asp
 290 295 300
 Tyr Val Cys Cys Ala Tyr Asn Asn Ile Thr Gly Arg Gln Asp Glu
 305 310 315
 Thr His Phe Thr Val Ile Ile Thr Ser Val Gly Leu Glu Lys Leu

| | | |
|---|-----|-----|
| 320 | 325 | 330 |
| Ala Gln Lys Gly Lys Ser Leu Ser Pro Leu Ala Ser Ile Thr Gly | | |
| 335 | 340 | 345 |
| Ile Ser Leu Phe Leu Ile Ile Ser Met Cys Leu Leu Phe Leu Trp | | |
| 350 | 355 | 360 |
| Lys Lys Tyr Gln Pro Tyr Lys Val Ile Lys Gln Lys Leu Glu Gly | | |
| 365 | 370 | 375 |
| Arg Pro Glu Thr Glu Tyr Arg Lys Ala Gln Thr Phe Ser Gly His | | |
| 380 | 385 | 390 |
| Glu Asp Ala Leu Asp Asp Phe Gly Ile Tyr Glu Phe Val Ala Phe | | |
| 395 | 400 | 405 |
| Pro Asp Val Ser Gly Val Ser Arg Ile Pro Ser Arg Ser Val Pro | | |
| 410 | 415 | 420 |
| Ala Ser Asp Cys Val Ser Gly Gln Asp Leu His Ser Thr Val Tyr | | |
| 425 | 430 | 435 |
| Glu Val Ile Gln His Ile Pro Ala Gln Gln Gln Asp His Pro Glu | | |
| 440 | 445 | 450 |

<210> 321
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 321
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<210> 322

<211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 322
 cactgacagg gttcctcacc cagg 24

<210> 323
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 323

ctccctctgg gctgtggagt atgtggggaa catgaccctg acatg 45

<210> 324

<211> 2397

<212> DNA

<213> Homo Sapien

<400> 324

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 acgttcgcgt catcacggac gagaactgga gagaactgct ggaaggagac 150
 tggatgatag aattttatgc ccctgggtgc cctgcttgctc aaaatcttca 200
 accggaatgg gaaagttttg ctgaatgggg agaagatctt gaggttaata 250
 ttgcgaaagt agatgtcaca gaggcagccag gactgagtgg acggtttatc 300
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 aagagtggaa gagtattgag cccgtttcat catggtttgg tccaggttct 450
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 catatactgt ttttgcttta gcaactctgt tttccggact gttattagga 600
 ctctgtatga tatttggtggc agattgcctt tgtccttcaa aaaggcgcag 650
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 aacctttgaa aaaagtggag gaggaacaag aggcggatga agaagatgtt 750
 tcagaagaag aagctgaaag taaagaagga acaaacaag actttccaca 800
 gaatgccata agacaacgct ctctgggtcc atcattggcc acagataaat 850
 cctagttaaa ttttatagtt atcttaatat tatgattttg ataaaaacag 900
 aagattgac attttgtttg gtttgaagtg aactgtgact tttttgaata 950
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<210> 326
<211> 23
<212> DNA

<213> Artificial Sequence

<220>
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<400> 326
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<210> 327
<211> 20
<212> DNA
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<223> Synthetic Oligonucleotide Probe

<400> 327
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<210> 328
<211> 21
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 328
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<210> 329
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<213> Artificial Sequence

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<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 326

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<210> 327

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<212> DNA

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 327

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<210> 328

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 328

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<210> 329

<211> 25

<212> DNA

<213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 329
 ttgaaggaca aaggcaatct gccac 25

<210> 330
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 330
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<210> 331
 <211> 2168
 <212> DNA
 <213> Homo Sapien

<400> 331
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 ggtttggtgt cctgagctgt gtgcaggccg aattcttcac ctctattggg 250
 cacatgactg acctgattta tgcagagaaa gagctggtgc agtctctgaa 300
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cctaccagaa aaaaaaaaaa 2168

<211> 533

<213> Homo Sapien

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Trp Ala Asn Lys Met Glu Ala Leu Thr Ser Lys Ser Ala Ala Asp
65 70 75

Lys Arg Leu Asn Thr Asp Trp Pro Ala Leu Glu Asp Leu Val Leu
95 100 105

Gln Phe Phe Pro Thr Asp Glu Asp Glu Ile Gly Ala Ala Lys Ala
125 130 135

Ser Arg Gly Glu Leu Pro Gly Thr Lys Tyr Gln Ala Met Leu Ser
155 160 165

Asp Tyr Tyr His Thr Val Leu Trp Met Glu Gln Val Leu Lys Gln
185 190 195

Leu Asp Ala Gly Glu Glu Ala Thr Thr Thr Lys Ser Gln Val Leu
200 205 210

| | | | | |
|-----------------|---|-----|-----|-----|
| Asp Tyr Leu Ser | Tyr Ala Val Phe Gln Leu Gly Asp Leu His Arg | 215 | 220 | 225 |
| Ala Leu Glu Leu | Thr Arg Arg Leu Leu Ser Leu Asp Pro Ser His | 230 | 235 | 240 |
| Glu Arg Ala Gly | Gly Asn Leu Arg Tyr Phe Glu Gln Leu Leu Glu | 245 | 250 | 255 |
| Glu Glu Arg Glu | Lys Thr Leu Thr Asn Gln Thr Glu Ala Glu Leu | 260 | 265 | 270 |
| Ala Thr Pro Glu | Gly Ile Tyr Glu Arg Pro Val Asp Tyr Leu Pro | 275 | 280 | 285 |
| Glu Arg Asp Val | Tyr Glu Ser Leu Cys Arg Gly Glu Gly Val Lys | 290 | 295 | 300 |
| Leu Thr Pro Arg | Arg Gln Lys Arg Leu Phe Cys Arg Tyr His His | 305 | 310 | 315 |
| Gly Asn Arg Ala | Pro Gln Leu Leu Ile Ala Pro Phe Lys Glu Glu | 320 | 325 | 330 |
| Asp Glu Trp Asp | Ser Pro His Ile Val Arg Tyr Tyr Asp Val Met | 335 | 340 | 345 |
| Ser Asp Glu Glu | Ile Glu Arg Ile Lys Glu Ile Ala Lys Pro Lys | 350 | 355 | 360 |
| Leu Ala Arg Ala | Thr Val Arg Asp Pro Lys Thr Gly Val Leu Thr | 365 | 370 | 375 |
| Val Ala Ser Tyr | Arg Val Ser Lys Ser Ser Trp Leu Glu Glu Asp | 380 | 385 | 390 |
| Asp Asp Pro Val | Val Ala Arg Val Asn Arg Arg Met Gln His Ile | 395 | 400 | 405 |
| Thr Gly Leu Thr | Val Lys Thr Ala Glu Leu Leu Gln Val Ala Asn | 410 | 415 | 420 |
| Tyr Gly Val Gly | Gly Gln Tyr Glu Pro His Phe Asp Phe Ser Arg | 425 | 430 | 435 |
| Arg Pro Phe Asp | Ser Gly Leu Lys Thr Glu Gly Asn Arg Leu Ala | 440 | 445 | 450 |
| Thr Phe Leu Asn | Tyr Met Ser Asp Val Glu Ala Gly Gly Ala Thr | 455 | 460 | 465 |
| Val Phe Pro Asp | Leu Gly Ala Ala Ile Trp Pro Lys Lys Gly Thr | 470 | 475 | 480 |

Ala Val Phe Trp Tyr Asn Leu Leu Arg Ser Gly Glu Gly Asp Tyr
485 490 495

Arg Thr Arg His Ala Ala Cys Pro Val Leu Val Gly Cys Lys Trp
500 505 510

Val Ser Asn Lys Trp Phe His Glu Arg Gly Gln Glu Phe Leu Arg
515 520 525

Pro Cys Gly Ser Thr Glu Val Asp
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<210> 333

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 333

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<210> 334

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 334

ggacccttct gtgtgccag 19

<210> 335

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 335

ggtctcaaga actcctgtc 19

<210> 336

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 336

acactcagca ttgcctggta cttg 24

<210> 337

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 337

gggcacatga ctgacctgat ttatgcagag aaagagctgg tgcag 45

<210> 338

<211> 2789

<212> DNA

<213> Homo Sapien

<400> 338

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<210> 339

<211> 772

<212> PRT

<213> Homo Sapien

<400> 339

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Leu | Ser | Ser | Leu | Leu | Ala | Leu | Leu | Arg | Pro | Ala | Leu | Pro |
| 1 | | | | 5 | | | | | 10 | | | | 15 | |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ile | Leu | Gly | Leu | Ser | Leu | Gly | Cys | Ser | Leu | Ser | Leu | Leu | Arg |
| | | | 20 | | | | | 25 | | | | | 30 | |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ser | Trp | Ile | Gln | Gly | Glu | Gly | Glu | Asp | Pro | Cys | Val | Glu | Ala |
| | | | 35 | | | | | 40 | | | | | 45 | |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Gly | Glu | Arg | Gly | Gly | Pro | Gln | Asn | Pro | Asp | Ser | Arg | Ala | Arg |
| | | | 50 | | | | | 55 | | | | | 60 | |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Asp | Gln | Ser | Asp | Glu | Asp | Phe | Lys | Pro | Arg | Ile | Val | Pro | Tyr |
| | | | 65 | | | | | 70 | | | | | 75 | |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Arg | Asp | Pro | Asn | Lys | Pro | Tyr | Lys | Lys | Val | Leu | Arg | Thr | Arg |
| | | | 80 | | | | | 85 | | | | | 90 | |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Ile | Gln | Thr | Glu | Leu | Gly | Ser | Arg | Glu | Arg | Leu | Leu | Val | Ala |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

| | | | | | |
|-----------------|---------------------|-------------------------|-----|--|-----|
| | 95 | | 100 | | 105 |
| Val Leu Thr Ser | Arg Ala Thr Leu Ser | Thr Leu Ala Val Ala Val | | | |
| | 110 | | 115 | | 120 |
| Asn Arg Thr Val | Ala His His Phe Pro | Arg Leu Leu Tyr Phe Thr | | | |
| | 125 | | 130 | | 135 |
| Gly Gln Arg Gly | Ala Arg Ala Pro Ala | Gly Met Gln Val Val Ser | | | |
| | 140 | | 145 | | 150 |
| His Gly Asp Glu | Arg Pro Ala Trp Leu | Met Ser Glu Thr Leu Arg | | | |
| | 155 | | 160 | | 165 |
| His Leu His Thr | His Phe Gly Ala Asp | Tyr Asp Trp Phe Phe Ile | | | |
| | 170 | | 175 | | 180 |
| Met Gln Asp Asp | Thr Tyr Val Gln Ala | Pro Arg Leu Ala Ala Leu | | | |
| | 185 | | 190 | | 195 |
| Ala Gly His Leu | Ser Ile Asn Gln Asp | Leu Tyr Leu Gly Arg Ala | | | |
| | 200 | | 205 | | 210 |
| Glu Glu Phe Ile | Gly Ala Gly Glu Gln | Ala Arg Tyr Cys His Gly | | | |
| | 215 | | 220 | | 225 |
| Gly Phe Gly Tyr | Leu Leu Ser Arg Ser | Leu Leu Leu Arg Leu Arg | | | |
| | 230 | | 235 | | 240 |
| Pro His Leu Asp | Gly Cys Arg Gly Asp | Ile Leu Ser Ala Arg Pro | | | |
| | 245 | | 250 | | 255 |
| Asp Glu Trp Leu | Gly Arg Cys Leu Ile | Asp Ser Leu Gly Val Gly | | | |
| | 260 | | 265 | | 270 |
| Cys Val Ser Gln | His Gln Gly Gln Gln | Tyr Arg Ser Phe Glu Leu | | | |
| | 275 | | 280 | | 285 |
| Ala Lys Asn Arg | Asp Pro Glu Lys Glu | Gly Ser Ser Ala Phe Leu | | | |
| | 290 | | 295 | | 300 |
| Ser Ala Phe Ala | Val His Pro Val Ser | Glu Gly Thr Leu Met Tyr | | | |
| | 305 | | 310 | | 315 |
| Arg Leu His Lys | Arg Phe Ser Ala Leu | Glu Leu Glu Arg Ala Tyr | | | |
| | 320 | | 325 | | 330 |
| Ser Glu Ile Glu | Gln Leu Gln Ala Gln | Ile Arg Asn Leu Thr Val | | | |
| | 335 | | 340 | | 345 |
| Leu Thr Pro Glu | Gly Glu Ala Gly Leu | Ser Trp Pro Val Gly Leu | | | |
| | 350 | | 355 | | 360 |

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Ala | Pro | Phe | Thr | Pro | His | Ser | Arg | Phe | Glu | Val | Leu | Gly | Trp | 365 | 370 | 375 |
| Asp | Tyr | Phe | Thr | Glu | Gln | His | Thr | Phe | Ser | Cys | Ala | Asp | Gly | Ala | 380 | 385 | 390 |
| Pro | Lys | Cys | Pro | Leu | Gln | Gly | Ala | Ser | Arg | Ala | Asp | Val | Gly | Asp | 395 | 400 | 405 |
| Ala | Leu | Glu | Thr | Ala | Leu | Glu | Gln | Leu | Asn | Arg | Arg | Tyr | Gln | Pro | 410 | 415 | 420 |
| Arg | Leu | Arg | Phe | Gln | Lys | Gln | Arg | Leu | Leu | Asn | Gly | Tyr | Arg | Arg | 425 | 430 | 435 |
| Phe | Asp | Pro | Ala | Arg | Gly | Met | Glu | Tyr | Thr | Leu | Asp | Leu | Leu | Leu | 440 | 445 | 450 |
| Glu | Cys | Val | Thr | Gln | Arg | Gly | His | Arg | Arg | Ala | Leu | Ala | Arg | Arg | 455 | 460 | 465 |
| Val | Ser | Leu | Leu | Arg | Pro | Leu | Ser | Arg | Val | Glu | Ile | Leu | Pro | Met | 470 | 475 | 480 |
| Pro | Tyr | Val | Thr | Glu | Ala | Thr | Arg | Val | Gln | Leu | Val | Leu | Pro | Leu | 485 | 490 | 495 |
| Leu | Val | Ala | Glu | Ala | Ala | Ala | Ala | Pro | Ala | Phe | Leu | Glu | Ala | Phe | 500 | 505 | 510 |
| Ala | Ala | Asn | Val | Leu | Glu | Pro | Arg | Glu | His | Ala | Leu | Leu | Thr | Leu | 515 | 520 | 525 |
| Leu | Leu | Val | Tyr | Gly | Pro | Arg | Glu | Gly | Gly | Arg | Gly | Ala | Pro | Asp | 530 | 535 | 540 |
| Pro | Phe | Leu | Gly | Val | Lys | Ala | Ala | Ala | Ala | Glu | Leu | Glu | Arg | Arg | 545 | 550 | 555 |
| Tyr | Pro | Gly | Thr | Arg | Leu | Ala | Trp | Leu | Ala | Val | Arg | Ala | Glu | Ala | 560 | 565 | 570 |
| Pro | Ser | Gln | Val | Arg | Leu | Met | Asp | Val | Val | Ser | Lys | Lys | His | Pro | 575 | 580 | 585 |
| Val | Asp | Thr | Leu | Phe | Phe | Leu | Thr | Thr | Val | Trp | Thr | Arg | Pro | Gly | 590 | 595 | 600 |
| Pro | Glu | Val | Leu | Asn | Arg | Cys | Arg | Met | Asn | Ala | Ile | Ser | Gly | Trp | 605 | 610 | 615 |
| Gln | Ala | Phe | Phe | Pro | Val | His | Phe | Gln | Glu | Phe | Asn | Pro | Ala | Leu | 620 | 625 | 630 |

Ser Pro Gln Arg Ser Pro Pro Gly Pro Pro Gly Ala Gly Pro Asp
 635 640 645
 Pro Pro Ser Pro Pro Gly Ala Asp Pro Ser Arg Gly Ala Pro Ile
 650 655 660
 Gly Gly Arg Phe Asp Arg Gln Ala Ser Ala Glu Gly Cys Phe Tyr
 665 670 675
 Asn Ala Asp Tyr Leu Ala Ala Arg Ala Arg Leu Ala Gly Glu Leu
 680 685 690
 Ala Gly Gln Glu Glu Glu Glu Ala Leu Glu Gly Leu Glu Val Met
 695 700 705
 Asp Val Phe Leu Arg Phe Ser Gly Leu His Leu Phe Arg Ala Val
 710 715 720
 Glu Pro Gly Leu Val Gln Lys Phe Ser Leu Arg Asp Cys Ser Pro
 725 730 735
 Arg Leu Ser Glu Glu Leu Tyr His Arg Cys Arg Leu Ser Asn Leu
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 Gln Glu Gln Ala Asn Ser Thr
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<211> 1572

<212> DNA

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 ctttttgaag ggtgtgatgc ttggaagcat tttctgtgct ttgatcacta 150
 tgctaggaca cattaggatt ggtcatggaa atagaatgca ccaccatgag 200
 catcatcacc tacaagctcc taacaaagaa gatattctga aaatttcaga 250
 ggatgagcgc atggagctca gtaagagctt tcgagtatac tgtattatcc 300
 ttgtaaaacc caaagatgtg agtctttggg ctgcagtaaa ggagacttgg 350
 accaaacact gtgacaaaagc agagttcttc agttctgaaa atgttaaagt 400

gtttgagtca attaatatgg acacaaatga catgtggtta atgatgagaa 450
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 tttgttaaaa aaggatccat cacagccttt ctatctaggc cacactataa 600
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 gtagaatcaa tgaaaagact taacagcctt ctcaatatcc cagaaaagtg 700
 tcctgaacag ggaggatga tttggaagat atctgaagat aaacagctag 750
 cagtttgcct gaaatatgct ggagtatttg cagaaaatgc agaagatgct 800
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 ggttttctta cctccaaatg gttctgacaa tgactgagaa gtggtagaaa 1050
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 gtaactacat atccaataca gctgtatggt tctttttctt ttctaatttg 1150
 gtggcactgg tataaccaca cattaaagtc agtagtacat ttttaaatga 1200
 ggggtggtttt tttcttttaa acacatgaac attgtaaatg tgttggaag 1250
 aagtgtttta agaataataa ttttgcaa atactattaa taaatattat 1300
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<210> 341

<211> 318

<212> PRT

<213> Homo Sapien

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| Met 1 | Leu | Ser | Glu | Ser 5 | Ser | Ser | Phe | Leu | Lys 10 | Gly | Val | Met | Leu | Gly 15 |
| Ser | Ile | Phe | Cys | Ala 20 | Leu | Ile | Thr | Met | Leu 25 | Gly | His | Ile | Arg | Ile 30 |
| Gly | His | Gly | Asn | Arg 35 | Met | His | His | His | Glu 40 | His | His | His | Leu | Gln 45 |
| Ala | Pro | Asn | Lys | Glu 50 | Asp | Ile | Leu | Lys | Ile 55 | Ser | Glu | Asp | Glu | Arg 60 |
| Met | Glu | Leu | Ser | Lys 65 | Ser | Phe | Arg | Val | Tyr 70 | Cys | Ile | Ile | Leu | Val 75 |
| Lys | Pro | Lys | Asp | Val 80 | Ser | Leu | Trp | Ala | Ala 85 | Val | Lys | Glu | Thr | Trp 90 |
| Thr | Lys | His | Cys | Asp 95 | Lys | Ala | Glu | Phe | Phe 100 | Ser | Ser | Glu | Asn | Val 105 |
| Lys | Val | Phe | Glu | Ser 110 | Ile | Asn | Met | Asp | Thr 115 | Asn | Asp | Met | Trp | Leu 120 |
| Met | Met | Arg | Lys | Ala 125 | Tyr | Lys | Tyr | Ala | Phe 130 | Asp | Lys | Tyr | Arg | Asp 135 |
| Gln | Tyr | Asn | Trp | Phe 140 | Phe | Leu | Ala | Arg | Pro 145 | Thr | Thr | Phe | Ala | Ile 150 |
| Ile | Glu | Asn | Leu | Lys 155 | Tyr | Phe | Leu | Leu | Lys 160 | Lys | Asp | Pro | Ser | Gln 165 |
| Pro | Phe | Tyr | Leu | Gly 170 | His | Thr | Ile | Lys | Ser 175 | Gly | Asp | Leu | Glu | Tyr 180 |
| Val | Gly | Met | Glu | Gly 185 | Gly | Ile | Val | Leu | Ser 190 | Val | Glu | Ser | Met | Lys 195 |
| Arg | Leu | Asn | Ser | Leu 200 | Leu | Asn | Ile | Pro | Glu 205 | Lys | Cys | Pro | Glu | Gln 210 |
| Gly | Gly | Met | Ile | Trp 215 | Lys | Ile | Ser | Glu | Asp 220 | Lys | Gln | Leu | Ala | Val 225 |
| Cys | Leu | Lys | Tyr | Ala 230 | Gly | Val | Phe | Ala | Glu 235 | Asn | Ala | Glu | Asp | Ala 240 |
| Asp | Gly | Lys | Asp | Val 245 | Phe | Asn | Thr | Lys | Ser 250 | Val | Gly | Leu | Ser | Ile 255 |
| Lys | Glu | Ala | Met | Thr | Tyr | His | Pro | Asn | Gln | Val | Val | Glu | Gly | Cys |

| | | | | | |
|---------------------|-------------------------|---------------------|-----|--|-----|
| | 260 | | 265 | | 270 |
| Cys Ser Asp Met | Ala Val Thr Phe Asn Gly | Leu Thr Pro Asn Gln | | | |
| | 275 | 280 | | | 285 |
| Met His Val Met | Met Tyr Gly Val Tyr Arg | Leu Arg Ala Phe Gly | | | |
| | 290 | 295 | | | 300 |
| His Ile Phe Asn Asp | Ala Leu Val Phe Leu | Pro Pro Asn Gly Ser | | | |
| | 305 | 310 | | | 315 |

Asp Asn Asp

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<210> 343

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ctggttcttc cttgcacg 18

<210> 344

<211> 28

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gcccaaagtc cctaaggcgg tataacccc 28

<210> 345

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<210> 346

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<400> 346

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<210> 347

<211> 18

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<210> 349

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<210> 357
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<210> 358
 <211> 47
 <212> DNA
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<210> 359
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<400> 359
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| Cys | Phe | Ser | Ser | Gln | Met | Phe | Leu | Trp | Thr | Val | Ala | Gly | Ile | Pro | |
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| Ile | Leu | Phe | Leu | Ser | Ala | Cys | Phe | Ile | Thr | Arg | Cys | Val | Val | Thr | |
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| Phe | Arg | Ile | Phe | Gln | Thr | Cys | Asp | Glu | Lys | Lys | Phe | Gln | Leu | Pro | |
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| Glu | Asn | Phe | Thr | Glu | Leu | Ser | Cys | Tyr | Asn | Tyr | Gly | Ser | Gly | Ser | |
| | | | | 65 | | | | | 70 | | | | | 75 | |
| Val | Lys | Asn | Cys | Cys | Pro | Leu | Asn | Trp | Glu | Tyr | Phe | Gln | Ser | Ser | |
| | | | | 80 | | | | | 85 | | | | | 90 | |
| Cys | Tyr | Phe | Phe | Ser | Thr | Asp | Thr | Ile | Ser | Trp | Ala | Leu | Ser | Leu | |
| | | | | 95 | | | | | 100 | | | | | 105 | |
| Lys | Asn | Cys | Ser | Ala | Met | Gly | Ala | His | Leu | Val | Val | Ile | Asn | Ser | |
| | | | | 110 | | | | | 115 | | | | | 120 | |
| Gln | Glu | Glu | Gln | Glu | Phe | Leu | Ser | Tyr | Lys | Lys | Pro | Lys | Met | Arg | |
| | | | | 125 | | | | | 130 | | | | | 135 | |
| Glu | Phe | Phe | Ile | Gly | Leu | Ser | Asp | Gln | Val | Val | Glu | Gly | Gln | Trp | |
| | | | | 140 | | | | | 145 | | | | | 150 | |
| Gln | Trp | Val | Asp | Gly | Thr | Pro | Leu | Thr | Lys | Ser | Leu | Ser | Phe | Trp | |
| | | | | 155 | | | | | 160 | | | | | 165 | |
| Asp | Val | Gly | Glu | Pro | Asn | Asn | Ile | Ala | Thr | Leu | Glu | Asp | Cys | Ala | |
| | | | | 170 | | | | | 175 | | | | | 180 | |

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| Met | Ala | Leu | Arg | Arg | Pro | Pro | Arg | Leu | Arg | Leu | Cys | Ala | Arg | Leu | 1 | 5 | 10 | 15 |
| Pro | Asp | Phe | Phe | Leu | Leu | Leu | Leu | Phe | Arg | Gly | Cys | Leu | Ile | Gly | 20 | 25 | 30 | |
| Ala | Val | Asn | Leu | Lys | Ser | Ser | Asn | Arg | Thr | Pro | Val | Val | Gln | Glu | 35 | 40 | 45 | |
| Phe | Glu | Ser | Val | Glu | Leu | Ser | Cys | Ile | Ile | Thr | Asp | Ser | Gln | Thr | 50 | 55 | 60 | |
| Ser | Asp | Pro | Arg | Ile | Glu | Trp | Lys | Lys | Ile | Gln | Asp | Glu | Gln | Thr | 65 | 70 | 75 | |
| Thr | Tyr | Val | Phe | Phe | Asp | Asn | Lys | Ile | Gln | Gly | Asp | Leu | Ala | Gly | 80 | 85 | 90 | |
| Arg | Ala | Glu | Ile | Leu | Gly | Lys | Thr | Ser | Leu | Lys | Ile | Trp | Asn | Val | 95 | 100 | 105 | |
| Thr | Arg | Arg | Asp | Ser | Ala | Leu | Tyr | Arg | Cys | Glu | Val | Val | Ala | Arg | 110 | 115 | 120 | |
| Asn | Asp | Arg | Lys | Glu | Ile | Asp | Glu | Ile | Val | Ile | Glu | Leu | Thr | Val | 125 | 130 | 135 | |
| Gln | Val | Lys | Pro | Val | Thr | Pro | Val | Cys | Arg | Val | Pro | Lys | Ala | Val | 140 | 145 | 150 | |
| Pro | Val | Gly | Lys | Met | Ala | Thr | Leu | His | Cys | Gln | Glu | Ser | Glu | Gly | 155 | 160 | 165 | |
| His | Pro | Arg | Pro | His | Tyr | Ser | Trp | Tyr | Arg | Asn | Asp | Val | Pro | Leu | 170 | 175 | 180 | |
| Pro | Thr | Asp | Ser | Arg | Ala | Asn | Pro | Arg | Phe | Arg | Asn | Ser | Ser | Phe | 185 | 190 | 195 | |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Leu | Asn | Ser | Glu | Thr | Gly | Thr | Leu | Val | Phe | Thr | Ala | Val | His |
| | | | | 200 | | | | | 205 | | | | | 210 |
| Lys | Asp | Asp | Ser | Gly | Gln | Tyr | Tyr | Cys | Ile | Ala | Ser | Asn | Asp | Ala |
| | | | | 215 | | | | | 220 | | | | | 225 |
| Gly | Ser | Ala | Arg | Cys | Glu | Glu | Gln | Glu | Met | Glu | Val | Tyr | Asp | Leu |
| | | | | 230 | | | | | 235 | | | | | 240 |
| Asn | Ile | Gly | Gly | Ile | Ile | Gly | Gly | Val | Leu | Val | Val | Leu | Ala | Val |
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| Leu | Ala | Leu | Ile | Thr | Leu | Gly | Ile | Cys | Cys | Ala | Tyr | Arg | Arg | Gly |
| | | | | 260 | | | | | 265 | | | | | 270 |
| Tyr | Phe | Ile | Asn | Asn | Lys | Gln | Asp | Gly | Glu | Ser | Tyr | Lys | Asn | Pro |
| | | | | 275 | | | | | 280 | | | | | 285 |
| Gly | Lys | Pro | Asp | Gly | Val | Asn | Tyr | Ile | Arg | Thr | Asp | Glu | Glu | Gly |
| | | | | 290 | | | | | 295 | | | | | 300 |
| Asp | Phe | Arg | His | Lys | Ser | Ser | Phe | Val | Ile | | | | | |
| | | | | 305 | | | | | 310 | | | | | |

200
 210
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